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Oct 3, 2002

DOCUMENT-IDENTIFIER: US 20020143159 A1

TITLE: BONE MORPHOGENETIC PROTEIN (BMP)-17 AND BMP-18 COMPOSITIONS

Summary of Invention Paragraph:

[0003] Human BMP-17 and BMP-18 appear to be human homologs of a murine protein called Lefty. The nucleotide and amino acid sequences of murine Lefty are described in Zhou et al., Nature, 361:543-547 (1993). The murine Lefty gene has been described as being expressed in the mouse node during gastrulation. A related human protein, designated endometrial bleeding associated factor [EBAF] was published in Kothapelli et al., J. Clin. Invest., 99:2342-2350 (1997).

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Entry information

Entry name **TGF4_HUMAN**
 Primary accession number **O00292**
 Secondary accession numbers **O75611 Q8NBQ9**
 Entered in Swiss-Prot in **Release 35, November 1997**
 Sequence was last modified in **Release 40, October 2001**
 Annotations were last modified in **Release 44, July 2004**

Name and origin of the protein

Protein name
 Synonyms

Transforming growth factor beta 4 [Precursor]
TGF-beta 4
Endometrial bleeding-associated factor
Left-right determination factor A
Lefty-A protein
Name: EBAF

Gene name

Synonyms: LEFTA, LEFTYA, TGFB4

From

Homo sapiens (Human) [TaxID: 9606]

Taxonomy

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

References

[1] SEQUENCE FROM NUCLEIC ACID.

TISSUE=Placenta;

MEDLINE=97298127;PubMed=9153275 [NCBI, ExPASy, EBI, Israel, Japan]

Kothapalli R., Buyuksal I., Wu S.-Q., Chegini N., Tabibzadeh S.;

"Detection of ebaf, a novel human gene of the transforming growth factor beta superfamily association of gene expression with endometrial bleeding.";

J. Clin. Invest. 99:2342-2350(1997).

[2] REVISIONS.

MEDLINE=99162193;PubMed=10053005 [NCBI, ExPASy, EBI, Israel, Japan]

Kothapalli R.;

Unpublished results, cited by: Kosaki K., Bassi M.T., Kosaki R., Lewin M., Belmont J., Schauer G.,

Casey B.; Am. J. Hum. Genet. 64:712-721(1999).

[3] SEQUENCE FROM NUCLEIC ACID, AND VARIANT L-R AXIS MALFORMATIONS ASN-342.

TISSUE=Placenta;

MEDLINE=99162193;PubMed=10053005 [NCBI, ExPASy, EBI, Israel, Japan]

Kosaki K., Bassi M.T., Kosaki R., Lewin M., Belmont J., Schauer G., Casey B.;

"Characterization and mutation analysis of human LEFTY A and LEFTY B, homologues of murine genes implicated in left-right axis development.";

Am. J. Hum. Genet. 64:712-721(1999).

[4] SEQUENCE FROM NUCLEIC ACID.

DOI=10.1038/ng1285;PubMed=14702039 [NCBI, ExPASy, EBI, Israel, Japan]

Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Yamamoto J.-I., Sugano S.;

"Complete sequencing and characterization of 21,243 full-length human cDNAs.";

Nat. Genet. 36:40-45(2004).

[5] SEQUENCE FROM NUCLEIC ACID.

TISSUE=Ovary;

DOI=10.1073/pnas.242603899;MEDLINE=22388257;PubMed=12477932 [NCBI, ExPASy, EBI, Israel, Japan]

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Comments

- **FUNCTION:** Required for left-right (L-R) asymmetry determination of organ systems in mammals. May play a role in endometrial bleeding.
- **SUBCELLULAR LOCATION:** Secreted.
- **TISSUE SPECIFICITY:** Mesenchymal cells of the endometrial stroma.
- **DEVELOPMENTAL STAGE:** Transiently expressed before and during menstrual bleeding.
- **PTM:** The processing of the protein may also occur at the second R-X-X-R site located at AA 132-135. Processing appears to be regulated in a cell-type specific manner.
- **DISEASE:** Defects in EBAF are the cause of left-right axis malformations (L-R axis malformation) [MIM:601877]. The defect includes left pulmonary isomerism, with cardiac anomalies characterized by complete atrioventricular canal defect and hypoplastic left ventricle, and interrupted inferior vena cava.
- **SIMILARITY:** Belongs to the TGF-beta family.

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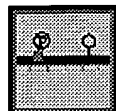
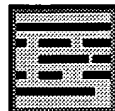
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AF081513; AAD48145.1; -. [\[EMBL / GenBank / DDBJ\]](#) [\[CoDingSequence\]](#)
 AK075344; BAC11556.1; -. [\[EMBL / GenBank / DDBJ\]](#) [\[CoDingSequence\]](#)
 BC035718; AAH35718.1; -. [\[EMBL / GenBank / DDBJ\]](#) [\[CoDingSequence\]](#)
 HSSP [P10600](#); 1TGJ. [\[HSSP ENTRY / PDB\]](#)
 Genew [HGNC:3122](#); EBAF.
 CleanEx [HGNC:3122](#); EBAF.
 GeneCards [EBAF](#).
 GeneLynx [EBAF](#); Homo sapiens.
 GenAtlas [EBAF](#).
 H-InvDB [HIX0001640](#); -.
 MIM [601877](#) [\[NCBI / EBI\]](#).
 GO [GO:0007275](#); Biological process: development (*traceable author statement*).
[GO:0007309](#); Biological process: oocyte axis determination (*traceable author statement*).
[GO:0007179](#); Biological process: transforming growth factor beta receptor signaling pathway (*traceable author statement*).
[QuickGo view](#).
 SOURCE [EBAF](#); Homo sapiens.
 Ensembl [O00292](#); Homo sapiens. [\[Entry / Contig view\]](#)
 InterPro [IPR001839](#); TGFb.
[IPR001111](#); TGFb_N.
[Graphical view of domain structure](#).
 Pfam [PF00019](#); TGF_beta; 1.
[PF00688](#); TGFb_propeptide; 1.
[Pfam graphical view of domain structure](#).
 ProDom [PD000357](#); TGFb; 1.
[\[Domain structure / List of seq. sharing at least 1 domain\]](#)
 PROSITE [PS00250](#); TGF_BETA_1; 1.
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 ProtoMap [O00292](#).
 PRESAGE [O00292](#).
 DIP [O00292](#).
 ModBase [O00292](#).
 SMR [O00292](#); 63A416CAE30F7A39.
 SWISS-2DPAGE [Get region on 2D PAGE](#).
 UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

Cytokine; **Developmental protein**; **Disease mutation**; **Glycoprotein**; **Growth factor**;
Multigene family; **Signal**.

Features

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Key	From	To	Length	Description	FTId
SIGNAL	<u>1</u>	<u>21</u>	21	Potential.	
PROPEP	<u>22</u>	<u>76</u>	55	Or 135 (Potential).	
CHAIN	<u>77</u>	<u>366</u>	290	Transforming growth factor beta 4.	
DISULFID	<u>251</u>	<u>264</u>		By similarity.	
DISULFID	<u>263</u>	<u>316</u>		By similarity.	
DISULFID	<u>293</u>	<u>351</u>		By similarity.	
DISULFID	<u>297</u>	<u>353</u>		By similarity.	
CARBOHYD	<u>158</u>	<u>158</u>		N-linked (GlcNAc...) (Potential).	
VARIANT	<u>342</u>	<u>342</u>	*	S -> N (in L-R axis malformations).	<u>VAR_010385</u>
CONFLICT	<u>183</u>	<u>183</u>		A -> P (in Ref. 4).	

Sequence informationLength: **366 AA** [This is the length of the unprocessed precursor]Molecular weight: **40920 Da** [This is the MW of the unprocessed precursor]CRC64: **63A416CAE30F7A39** [This is a checksum on the sequence]

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MWPLWLCWAL	WVLPLAGPGA	ALTEEQLLGS	LLRQLQLSEV	PVLDRADMEK	LVIPAHVRAQ
70	80	90	100	110	120
YVLLRRSHG	DRSRGKRFSQ	SFREYAGRFL	ASEASTHLLV	FGMEQRLPPN	SELVQAVLRL
130	140	150	160	170	180
FQEPVPKAAL	HRHGRLSPRS	AQARVTVEWL	RVRDDGSNRT	SLIDSRLVSV	HESGWKAFDV
190	200	210	220	230	240
TEAVNFWQQL	SRPRQPLLQ	VSVQREHLGP	LASGAHKLVR	FASQGAPAGL	GEPQLELHTL
250	260	270	280	290	300
DLRDYGAQGD	CDPEAPMTEG	TRCCRQEMYI	DLQGMKWAKN	WVLEPPGFLA	YECVGTCQQP
310	320	330	340	350	360
PEALAFNWP	LGPRQCIASE	TASLPMIVSI	KEGGRTRPQV	VSLPNMRVQK	CSCASDGALV

PRRLQP

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CLUSTAL FORMAT for T-COFFEE Version_1.37, CPU=0.00 sec, SCORE=18430, Nseq=2, Len=366

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unk|VIRT9911|Blast_submission  MWPLWLCWALWVLPLAGPGAALTEEQLLGSLLRQLQLSEVPVLDRADMEKLVIP
sp|O75610|LFTB_HUMAN          MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIP
                               * *****.***** *****.***.*****.*****

unk|VIRT9911|Blast_submission  YVLLRRSHGDRSRGKRFSQSFRVAGRFLASEASTHLLVFGMEQRLPPNSELV
sp|O75610|LFTB_HUMAN          YVALLQRSHGDRSRGKRFSQSFRVAGRFLALEASTHLLVFGMEQRLPPNSELV
                               **.***.***** *****

unk|VIRT9911|Blast_submission  FQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSLIDSRLSVHESG
sp|O75610|LFTB_HUMAN          FQEPVPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLSVHESG
                               *****.*****

unk|VIRT9911|Blast_submission  TEAVNFWQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQ
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                               *****

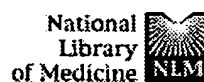
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sp|O75610|LFTB_HUMAN          DLGDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWWLEPPGFLAYECV
                               ** *****.*****

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                               *****.*****

unk|VIRT9911|Blast_submission  PRRLQP
sp|O75610|LFTB_HUMAN          PRRLQP
                               *****

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Multiple forms of TGF-beta: distinct promote differential expression.

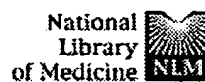
Roberts AB, Kim SJ, Noma T, Glick AB, Lafyatis R, Jakowlew SB, Geiser A, O'Reilly MA, Danielpour D,

Laboratory of Chemoprevention, National Cancer Instit MD 20892.

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There are now five known distinct isoforms of TGF-beta identity. Of these, only TGF-beta 1, 2 and 3 thus far ha demonstrated to be expressed in mammalian tissues; TG been described only in chicken and TGF-beta 5 only in f the biological activities of these five isoforms of TGF-b indistinguishable in most in vitro assays their sites of sy localization in vivo are often distinct. Expression of the isoforms is differentially controlled both in vivo, as in d and in vitro after treatment of cells with steroids, such or tamoxifen, or with retinoids. To investigate the basis observations we have cloned and characterized the prom human TGF-beta 1, 2 and 3 genes. Significant differenc found: whereas the TGF-beta 1 promoter has no TATAA regulated principally by AP-1 sites, both the TGF-beta 2 promoters have TATAA boxes as well as AP-2 sites and

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Transforming growth factor beta 1 expressior endometrium of the mare during placentation.

Lennard SN, Stewart F, Allen WR.

Thoroughbred Breeders' Association Equine Fertility U
Paddocks, Suffolk, United Kingdom.

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In situ hybridization, Northern blotting, and immunohist techniques were used to study the expression of transfactor beta 1 (TGF beta 1) in the endometrium of the m first 150 days of pregnancy (term = 330-340 days). In s hybridization using an oligonucleotide (45mer) probe, ba homologous region within all known mammalian TGF beta sequences, demonstrated TGF beta 1 mRNA accumulatio glandular and luminal epithelial cells of the endometrium onwards which corresponds to the time of implantation Expression in the endometrium remained at a high level the sampling period (day 150). There was also marked ex TGF beta 1 in the mononuclear cells accumulated around of the specialized trophoblast cells of the endometrial endometrium and in the mononuclear cells accumulated i endometrial stroma of mares carrying failing donkey-in-pregnancies created by embryo transfer. The sense (co oligonucleotide probe exhibited no hybridization to any

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stage. Northern blot analysis demonstrated that the oli probe and a porcine TGF beta 1 cDNA clone hybridized kb transcript in horse endometrial and lymphocyte RNA validating the oligonucleotide probe for detection of ho mRNA. Furthermore, both probes demonstrated an incr the pregnant endometrium from day 33 onwards, thereb the in situ hybridization results. Immunostaining with a anti-bovine TGF beta 1 serum also showed increasing TG accumulation in endometrial epithelia during pregnancy, of the protein in endometrial stroma and in the trophob the placenta after day 60 of pregnancy. These results s beta 1 expression increases in the maternal endometrium at the time of implantation and that it may play a role in endometrial and/or trophoblast growth and differentiat placentation in this species. It may also influence fetal (via placental transfer) at a later stage of gestation.

PMID: 8562058 [PubMed - indexed for MEDLINE]

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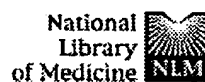
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- Nature. 1996 May 9;381(6578):116-7.
- Nature. 1997 Jan 9;385(6612):111-2.

Left-right asymmetric expression of the TGF member lefty in mouse embryos.

Meno C, Saijoh Y, Fujii H, Ikeda M, Yokoyama T, Y Toyoda Y, Hamada H.

PubMed
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Tokyo Metropolitan Institute of Medical Science, Japan

Examples of lateral asymmetry are often found in vertebrate the heart being on the left side, but the molecular mechanism governing the establishment of this left-right (L-R) has been unknown. A diffusible morphogen may determine L-R polarity. A likely molecule has not so far been identified. Here we report the gene lefty, a member of the transforming growth factor- β family which may encode a morphogen for L-R determination. Lefty contains the cysteine-knot motif characteristic of this family and is secreted as a processed form of relative molecular mass 25K-32K. Surprisingly, lefty is expressed in the left half of gastrulating mouse embryos. This asymmetric expression is transient and occurs just before the first sign of lateralization appears. In the mouse mutants iv and inv, which cause severe

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the sites of lefty expression are inverted, indicating th
downstream of iv and inv. These results suggest that lef
involved in setting up L-R asymmetry in the organ system

PMID: 8610011 [PubMed - indexed for MEDLINE]

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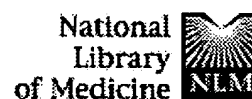
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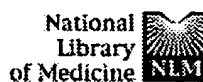
Transforming growth factor beta 1 expression in the endometrium during placentation.

Lennard SN, Stewart F, Allen WR.

Thoroughbred Breeders' Association Equine Fertility Unit, Mertoun Paddock United Kingdom.

In situ hybridization, Northern blotting, and immunohistochemical technique study the expression of transforming growth factor beta 1 (TGF beta 1) in the endometrium of the mare during the first 150 days of pregnancy (term = 330-340 days). In situ hybridization using an oligonucleotide (45mer) probe, based on a homologous sequence within all known mammalian TGF beta 1 DNA sequences, demonstrated TGF beta 1 mRNA accumulation in the glandular and luminal epithelial cells of the endometrium from day 33 onwards which corresponds to the time of implantation (day 33-45). Expression in the endometrium remained at a high level to the end of the pregnancy (day 150). There was also marked expression of TGF beta 1 in the mononuclear cells accumulated around the periphery of the specialized trophoblast cells of the decidua within the endometrium and in the mononuclear cells accumulated in the stroma of mares carrying failing donkey-in-horse pregnancies created by embryo transfer. The sense (control) oligonucleotide probe exhibited no hybridization to any tissue. Northern blot analysis demonstrated that the oligonucleotide probe and TGF beta 1 cDNA clone hybridized to a single 2.5 kb transcript in horse endometrial lymphocyte RNA, thus validating the oligonucleotide probe for detection of TGF beta 1 mRNA. Furthermore, both probes demonstrated an increased signal in the endometrium from day 33 onwards, thereby confirming the in situ hybridization results. Immunostaining with a specific anti-bovine TGF beta 1 serum also showed increased TGF beta 1 accumulation in endometrial epithelia during pregnancy, and localized the protein in endometrial stroma and in the trophoblast layer of the placenta of pregnancy. These results show that TGF beta 1 expression increases in the endometrium of the mare at the time of implantation and that it may play a role in regulating endometrial and/or trophoblast growth and differentiation during pregnancy in this species. It may also influence fetal development (via placental transfer) during pregnancy.

PMID: 8562058 [PubMed - indexed for MEDLINE]



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Cytokine expression in human endometrium throughout the menstrual cycle.

Tabibzadeh S, Sun XZ.

Department of Pathology, University of South Florida Health Center, Tampa 33612.

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Recent evidence suggests that diverse endometrial functions are regulated by cytokines. In this report, the presence of mRNA of cytokines were studied in human endometrium throughout the menstrual cycle. The presence of the interleukin-1 (interleukin-1 (IL-1) beta, interleukin receptor antagonist interleukin-6 (IL-6) and transforming growth factor (TGF) proteins were demonstrated by immunohistochemical staining. IL-1 alpha and TGF-alpha proteins were strongly expressed. beta protein was weakly expressed in all the cells in the endometrium as epithelial cells. IRAP was markedly expressed in the endometrium. The morphological features of macrophages scattered in the endometrium. The expression of IL-6 protein was predominant in the endometrium. Diffuse cytoplasmic expression of IL-1 alpha in the endometrial epithelium during the proliferative phase correlated with its enhanced luminal expression during the secretory phase of the menstrual cycle. In addition, the presence of these cytokines in endometrium was established through

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entire menstrual cycle by reverse transcription-polymer reaction (RT-PCR). Abundant expression of cytokines in endometrium emphasizes the significant roles that cyto cell-cell interactions and in regulating endometrial funct

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09393628 PMID: 1353860

Correction: a new interpretation of a chicken transforming growth factor-beta 4 complementary DNA.

Burt D W ; Jakowlew S B

Department of Cellular and Molecular Biology, Edinburgh Research Station,
Roslin, Midlothian, United Kingdom.

Molecular endocrinology (Baltimore, Md.) (UNITED STATES) Jun 1992 ,
6 (6) p989-92, ISSN 0888-8809 Journal Code: 8801431

Document type: Journal Article

Languages: ENGLISH

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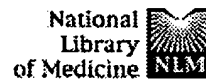
Descriptors: *Chickens--genetics--GE; *DNA--genetics--GE; *Protein
Precursors--genetics--GE; *Transforming Growth Factor beta--genetics--GE;
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Protein Sorting Signals--genetics--GE; Sequence Homology, Nucleic Acid;
Species Specificity

Molecular Sequence Databank No.: GENBANK/X08012

CAS Registry No.: 0 (Protein Precursors); 0 (Protein Sorting Signals)
; 0 (Transforming Growth Factor beta); 110343-45-8 (transforming growth
factor beta precursor); 9007-49-2 (DNA)

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Immunochemical study of transforming growth in the kidney of the rat and chicken.

Diaz-Ruiz C, Montaner B, Perez-Tomas R.

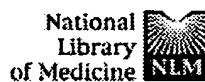
Department de Biologia Cellular i Anatomia Patologica, L (Barcelona), Spain.

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Transforming growth factor-beta (TGF-beta) is a homo polypeptide of 25 kDa, which regulates cell growth and and influences extracellular matrix metabolism. Using im techniques, we identified TGF-beta in the loops of Henl collecting and Bellini ducts of rat kidney and in the loop chicken kidney. Furthermore, we detected two TGF-beta-immunoreactive proteins on kidney blots of th and 47 kDa, and three on chicken kidney blots of 12.5, 3 We suggest that the precursor forms of rat and chicke or beta 3, chicken TGF-beta 4, and the mature form of expressed in the collecting and Bellini ducts of rat kidne loops of Henle of rat and chicken kidney.

PMID: 8791107 [PubMed - indexed for MEDLINE]

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☐ 1: Mol Endocrinol. 1992 Jun;6(6):989-92. Related

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Correction: a new interpretation of a chicken growth factor-beta 4 complementary DNA.

Burt DW, Jakowlew SB.

Department of Cellular and Molecular Biology, Edinburgh Station, Roslin, Midlothian, United Kingdom.

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PMID: 1353860 [PubMed - indexed for MEDLINE]

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L3: Entry 1 of 8

File: USPT

Nov 18, 2003

US-PAT-NO: 6649588

DOCUMENT-IDENTIFIER: US 6649588 B1

TITLE: Inhibition of TGF-.beta. and uses thereof

DATE-ISSUED: November 18, 2003

US-CL-CURRENT: 514/2; 514/21, 514/899, 530/350 *4*INT-CL: [07] A61 K 38/00, A01 N 25/00, C07 K 17/00

1, 14, 15
abnormal
uterine bleeding
menstrual bleed

L3: Entry 2 of 8

File: USPT

Aug 6, 2002

US-PAT-NO: 6428966

DOCUMENT-IDENTIFIER: US 6428966 B1**** See image for Certificate of Correction ****TITLE: Growth differentiation factor, lefty-1 *See*

DATE-ISSUED: August 6, 2002

US-CL-CURRENT: 435/7.1; 435/252.3, 435/254.11, 435/320.1, 435/325, 435/7.7,
435/7.9, 530/350, 530/351, 530/387.1, 530/387.9, 530/388.1, 530/388.23, 530/388.24,
530/389.1, 530/389.2, 536/23.1, 536/23.5 *[Signature]*INT-CL: [07] C07 K 14/475, C12 N 1/21, C12 N 5/10, C12 N 15/19, C12 N 15/63

L3: Entry 3 of 8

File: USPT

Sep 25, 2001

US-PAT-NO: 6294662

DOCUMENT-IDENTIFIER: US 6294662 B1

TITLE: Nucleic acids encoding an endometrial bleeding associated factor (ebaf)

DATE-ISSUED: September 25, 2001

US-CL-CURRENT: 536/23.5; 435/6, 536/23.1, 536/24.31, 536/24.33 *[Signature]*INT-CL: [07] C07 H 21/04, C12 Q 1/68

L3: Entry 4 of 8

File: USPT

Jun 29, 1999

US-PAT-NO: 5916751

DOCUMENT-IDENTIFIER: US 5916751 A

TITLE: Method for the diagnosis of selected adenocarcinomas

DATE-ISSUED: June 29, 1999

435/6
435/7.23
436/64
436/813

US-CL-CURRENT: 435/6; 435/7.23, 436/64, 436/813

INT-CL: [06] G01 N 33/574, G01 N 33/48, C12 Q 1/68

L3: Entry 5 of 8

File: DWPI

Nov 18, 2003

DERWENT-ACC-NO: 2002-352240

ABSTRACTED-PUB-NO: WO 200229105A

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TITLE: Inhibiting the activity of transforming growth factor (TGF) beta, for treating e.g. fibrosis, comprises contacting tissue expressing TGF beta with ebaf peptide its analogue

INT-CL (IPC): A01 N 25/00, A01 N 37/18, A61 K 38/00, C07 K 1/00, C07 K 14/00, C07 K 17/00, C12 Q 1/68, G01 N 33/574

Derwent-CL (DC): B01, B04, B05, D16

CPI Codes: B04-E03F; B04-E08; B04-F11; B04-H06F; B04-N02; B14-F01; B14-F08; B14-G02D; B14-H01; B14-J05E; B14-L06; B14-N12; B14-N14; B14-N17A; B14-N17B; B14-S03; D05-H12A; D05-H12E; D05-H12F;

L3: Entry 6 of 8

File: DWPI

Sep 25, 2001

DERWENT-ACC-NO: 2001-647266

ABSTRACTED-PUB-NO: US 6294662B

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TITLE: New nucleic acid molecule encoding endometrial bleeding associated factor, useful in early diagnosis of selected adenocarcinomas in human, e.g. adenocarcinomas of colon, ovaries or testis

INT-CL (IPC): C07 H 21/04, C12 Q 1/68

Derwent-CL (DC): B04, D16

CPI Codes: B04-E03F; B04-E05; B11-C08E5; B12-K04A1; D05-H09; D05-H12A; D05-H12D1;

L3: Entry 7 of 8

File: DWPI

Jun 29, 1999

DERWENT-ACC-NO: 1999-384717

ABSTRACTED-PUB-NO: US 5916751A

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TITLE: Detecting serous or mucinous colon/ovarian adenocarcinomas and testicular adenocarcinoma by assaying for elevated expression of a gene

INT-CL (IPC): C12 Q 1/68, G01 N 33/48, G01 N 33/574

Derwent-CL (DC): B04, D16, S03

CPI Codes: B04-B04C2; B04-B04L; B04-E01; B04-E05; B04-G02; B04-G21; B04-H01; B11-C07A; B11-C08E5; B12-K04A1; B12-K04F; D05-H09;

EPI Codes: S03-E14H1; S03-E14H4; S03-E14H6;

L3: Entry 8 of 8

File: DWPI

Jan 30, 2003

DERWENT-ACC-NO: 1999-153704

ABSTRACTED-PUB-NO: US 6428966B

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 Mol Endocrinology
 1996: 10: 1000-1009

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L9: Entry 1 of 2

File: USPT

Aug 6, 2002

US-PAT-NO: 6428966

DOCUMENT-IDENTIFIER: US 6428966 B1

**** See image for Certificate of Correction ****

TITLE: Growth differentiation factor, lefty-1

DATE-ISSUED: August 6, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Lee; Se-Jin	Baltimore	MD		
Huynh; Thanh	Baltimore	MD		
Sebald; Suzanne	Jessup	MD		

ASSIGNEE-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY	TYPE	CODE
The Johns Hopkins University School of Medicine	Baltimore	MD			02	

APPL-NO: 09/ 485053 [PALM]

DATE FILED: January 31, 2000

PARENT-CASE:

This application is an application filed under 35 U.S.C. 371 from PCT/US98/15352, filed Jul. 24, 1998 which claims benefit from U.S. Provisional application 60/054,382 filed Jul. 31, 1997, both of which are incorporated by reference in their entirety.

PCT-DATA:

APPL-NO	DATE-FILED	PUB-NO	PUB-DATE	371-DATE	102(E)-DATE
PCT/US98/15352	July 24, 1998	WO99/06444	Feb 11, 1999	Mar 5, 2000	Mar 5, 2000

INT-CL: [07] C07 K 14/475, C12 N 1/21, C12 N 5/10, C12 N 15/19, C12 N 15/63

US-CL-ISSUED: 435/7.1; 435/7.7, 435/7.9, 435/320.1, 435/325, 435/252.3, 435/254.11, 530/350, 530/351, 530/387.1, 530/387.9, 530/388.1, 530/388.23, 530/388.24, 530/389.1, 530/389.2, 536/23.1, 536/23.5

US-CL-CURRENT: 435/7.1; 435/252.3, 435/254.11, 435/320.1, 435/325, 435/7.7, 435/7.9, 530/350, 530/351, 530/387.1, 530/387.9, 530/388.1, 530/388.23, 530/388.24, 530/389.1, 530/389.2, 536/23.1, 536/23.5

FIELD-OF-SEARCH: 536/23.1, 536/23.5, 435/320.1, 435/325, 435/252.3, 435/7.1, 435/7.7, 435/7.9, 435/254.11, 530/387.1, 530/350, 530/387.9, 530/388.1, 530/388.23, 530/254.11, 530/388.24, 530/389.1, 530/389.2, 530/351

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<input type="checkbox"/>	<u>5350836</u>	September 1994	Kopchick et al.	
<input type="checkbox"/>	<u>6027917</u>	February 2000	Celeste et al.	

OTHER PUBLICATIONS

Vukicevic et al., 1996, PNAS USA 93:9021-9026.*
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Yoshioka, Hidefumi et al., "Pitx2, a Bicoid-Type Homeobox Gene, Is Involved in a Lefty-Signaling Pathway in Determination to Left-Right Asymmetry," Cell 94:299-305, 1998.

ART-UNIT: 1646

PRIMARY-EXAMINER: Kemmerer; Elizabeth

ATTY-AGENT-FIRM: Gary Cary Ware & Freidenrich LLP Haile; Lisa A.

ABSTRACT:

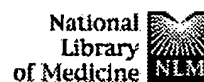
Growth differentiation factor Lefty-1 polypeptide and polynucleotides are provided herein. Also disclosed are diagnostic and therapeutic methods of using the Lefty-1 polypeptide and polynucleotide sequences.

22 Claims, 1 Drawing figures

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L2: Entry 1 of 2

File: USPT

Jan 27, 2004

US-PAT-NO: 6683156

DOCUMENT-IDENTIFIER: US 6683156 B1

** See image for Certificate of Correction **

TITLE: Method for diagnosing selected adenocarcinomas

DATE-ISSUED: January 27, 2004

US-CL-CURRENT: 530/350; 530/351, 530/399, 536/23.1, 536/23.5INT-CL: [07] C07 K 17/00, C07 H 21/04*Compositional*
4

L2: Entry 2 of 2

File: DWPI

Jan 27, 2004

DERWENT-ACC-NO: 2004-118581

ABSTRACTED-PUB-NO: US 6683156B

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TITLE: New endometrial bleeding associated factor protein, useful for diagnosing a mucinous adenocarcinoma of the ovaries or colon in a female human or of the testis or colon of a male human

INT-CL (IPC): C07 H 21/04, C07 K 17/00

Derwent-CL (DC): B04, D16

CPI Codes: B04-C01G; B04-E03F; B04-N02A0E; B11-C08F4; B12-K04A1; D05-H09; D05-H12A;

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TITLE: A new growth differentiation factor, Lefty-1 - useful to detect and treat cell proliferative and immunological disorders

INT-CL (IPC): A61 K 38/18, C07 K 14/475, C07 K 16/22, C12 N 1/21, C12 N 5/06, C12 N 5/10, C12 N 15/12, C12 N 15/19, C12 N 15/63, C12 P 21/02, G01 N 33/48, G01 N 33/53

Derwent-CL (DC): B04, D16 , S03

CPI Codes: B04-C01; B04-E08; B04-F0100E; B04-G02; B04-H06; B12-K04A1; B12-K04A3; B14-G03; B14-H01; B14-H01B; B14-N17A; B14-P01; D05-H09; D05-H11; D05-H12A; D05-H12E; D05-H14; D05-H17A2;

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NCBI BLAST program reference [PMID:9254694]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

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 Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]
 Database: EXPASY/UniProt
 1,621,919 sequences; 518,174,383 total letters

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List of potentially matching sequences

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<input type="checkbox"/>	tr	Q8MJV5	Bone morphogenetic protein 4 [sBmp4] [Suncus murinus (...	59	2e-07
<input type="checkbox"/>	sp	P49001	BMP2_RAT Bone morphogenetic protein 2 precursor (BMP-2...	57	4e-07
<input type="checkbox"/>	sp	P21274	BMP2_MOUSE Bone morphogenetic protein 2 precursor (BMP...	57	4e-07
<input type="checkbox"/>	tr	Q90YD7	Bone morphogenetic protein 2 (BMP-2) [BMP-2] [Xenopus ...	57	4e-07
<input type="checkbox"/>	tr	Q90YD6	Bone morphogenetic protein 4 [BMP-4] [Xenopus tropical...	57	4e-07
<input type="checkbox"/>	tr	Q6PAF3	LOC397874 protein [LOC397874] [Xenopus laevis (African...	57	7e-07

<input type="checkbox"/>	tr	Q91703	Bone morphogenetic protein 4 [BMP-4] [Xenopus laevis (...]	57	7e-07
<input type="checkbox"/>	tr	Q9MZV5	Bone morphogenetic protein 4 (Fragment) [bmp4] [Canis ...]	57	7e-07
<input type="checkbox"/>	sp	P12644	BMP4_HUMAN Bone morphogenetic protein 4 precursor (BMP...	56	9e-07
<input type="checkbox"/>	tr	Q6J3S6	Bone morphogenetic protein 24A [BMP24A] [Petromyzon ma...]	56	9e-07
<input type="checkbox"/>	tr	O73818	Bone morphogenetic protein 4 [BMP-4] [Xenopus laevis (...]	56	9e-07
<input type="checkbox"/>	tr	Q9U418	Bone morphogenetic protein 2/4 [BMP2/4] [Branchiostoma...]	56	1e-06
<input type="checkbox"/>	sp	O46576	BMP4_RABIT Bone morphogenetic protein 4 precursor (BMP...	55	2e-06
<input type="checkbox"/>	sp	P30885	BMP4_XENLA Bone morphogenetic protein 4 precursor (BMP...	55	2e-06
<input type="checkbox"/>	tr	Q90Y82	LjBmp2/4a (Fragment) [LjBmp2/4a] [Lampetra japonica (J...]	55	2e-06
<input type="checkbox"/>	tr	O96504	Bone morphogenetic protein 2/4 [AmphiBMP2/4] [Branchio...]	55	2e-06
<input type="checkbox"/>	sp	Q29607	BMP4_DAMDA Bone morphogenetic protein 4 precursor (BMP...	54	3e-06
<input type="checkbox"/>	tr	Q9U5E8	Pf-BMP2/4 [Pf-bmp2/4] [Ptychodera flava]	54	3e-06
<input type="checkbox"/>	sp	O46564	BMP2_RABIT Bone morphogenetic protein 2 precursor (BMP...	54	4e-06
<input type="checkbox"/>	sp	O19006	BMP2_DAMDA Bone morphogenetic protein 2 precursor (BMP...	54	4e-06
<input type="checkbox"/>	tr	Q9PVK1	Anti-dorsalizing morphogenetic protein [ADMP] [Gallus ...]	54	4e-06
<input type="checkbox"/>	sp	P30884	BMPB_XENLA Bone morphogenetic protein 2-II precursor (...]	53	8e-06
<input type="checkbox"/>	tr	Q9VQG9	CG16987-PA (Cg16987-pb) (GH14433p) [Alp23B] [Drosophil...]	53	8e-06
<input type="checkbox"/>	sp	O08717	IHBE_MOUSE Inhibin beta E chain precursor (Activin bet...]	53	1e-05
<input type="checkbox"/>	sp	P12643	BMP2_HUMAN Bone morphogenetic protein 2 precursor (BMP...	53	1e-05
<input type="checkbox"/>	tr	Q91XH3	Inhibin beta E [Inhbe] [Mus musculus (Mouse)]	53	1e-05
<input type="checkbox"/>	tr	Q7Q3Q7	AgCP11289 (Fragment) [agCG50272] [Anopheles gambiae st...]	53	1e-05
<input type="checkbox"/>	tr	Q6PUC6	Decapentaplegic (Fragment) [Anopheles gambiae (African...]	53	1e-05
<input type="checkbox"/>	tr	Q9W6T9	Activin beta B protein (Fragment) [inhbb] [Brachydanio...]	52	2e-05
<input type="checkbox"/>	tr	Q9PWR8	Activin beta B subunit precursor [Carassius auratus (G...]	52	2e-05
<input type="checkbox"/>	tr	Q869H8	GDF2 precursor [Crassostrea gigas (Pacific oyster)]	52	2e-05
<input type="checkbox"/>	tr	Q8MKC2	Bone morphogenetic protein 2 (Fragment) [Ovis aries (S...]	52	2e-05
<input type="checkbox"/>	tr	Q8MXZ3	Bone morphogenetic protein [HpBMP] [Hemicentrotus pulc...]	52	2e-05
<input type="checkbox"/>	tr	Q8IAE3	Sj-BMP2/4 [Sj-bmp2/4] [Stichopus japonicus (Sea cucumb...]	51	3e-05
<input type="checkbox"/>	tr	Q6XDQ0	Bone morphogenetic protein 2 [Gallus gallus (Chicken)]	50	5e-05
<input type="checkbox"/>	sp	P27093	IHBB_CHICK Inhibin beta B chain precursor (Activin bet...]	50	6e-05
<input type="checkbox"/>	tr	O13109	BMP2 [bmp2a] [Brachydanio rerio (Zebrafish) (Danio rer...]	50	6e-05
<input type="checkbox"/>	sp	O88959	IHBE_RAT Inhibin beta E chain precursor (Activin beta-...]	50	8e-05
<input type="checkbox"/>	sp	P17491	IHBB_RAT Inhibin beta B chain precursor (Activin beta-...]	50	8e-05
<input type="checkbox"/>	sp	Q04999	IHBB_MOUSE Inhibin beta B chain precursor (Activin bet...]	50	8e-05
<input type="checkbox"/>	sp	O95393	BM10_HUMAN Bone morphogenetic protein 10 precursor (BM...]	50	8e-05
<input type="checkbox"/>	sp	P48969	DVR1_STRPU DVR-1 protein homolog precursor [DVR1] [Str...]	49	1e-04
<input type="checkbox"/>	tr	Q90261	Activin beta B [inhbb] [Brachydanio rerio (Zebrafish) ...]	49	1e-04
<input type="checkbox"/>	tr	Q869H7	GDF3 precursor (Fragment) [Crassostrea gigas (Pacific ...]	49	1e-04
<input type="checkbox"/>	sp	P09529	IHBB_HUMAN Inhibin beta B chain precursor (Activin bet...]	49	2e-04
<input type="checkbox"/>	tr	Q9PTF9	Bone morphogenetic protein 7 [bmp7] [Brachydanio rerio...]	49	2e-04
<input type="checkbox"/>	tr	Q6EH35	Bone morphogenetic protein 2 (Fragment) [BMP-2] [Trach...]	49	2e-04
<input type="checkbox"/>	sp	P58166	IHBE_HUMAN Inhibin beta E chain precursor (Activin bet...]	48	2e-04
<input type="checkbox"/>	sp	Q9R229	BM10_MOUSE Bone morphogenetic protein 10 precursor (BM...]	48	2e-04
<input type="checkbox"/>	sp	Q24735	60A_DROVI 60A protein precursor (Glass bottom boat pro...]	48	2e-04
<input type="checkbox"/>	tr	Q9DGF1	Inhibin/activin (Fragment) [Cyprinus carpio (Common ca...]	48	2e-04

Graphical overview of the alignments

[Click here](#)

to resubmit your query after masking regions matching [PROSITE](#) profiles
or [Pfam](#) HMMs

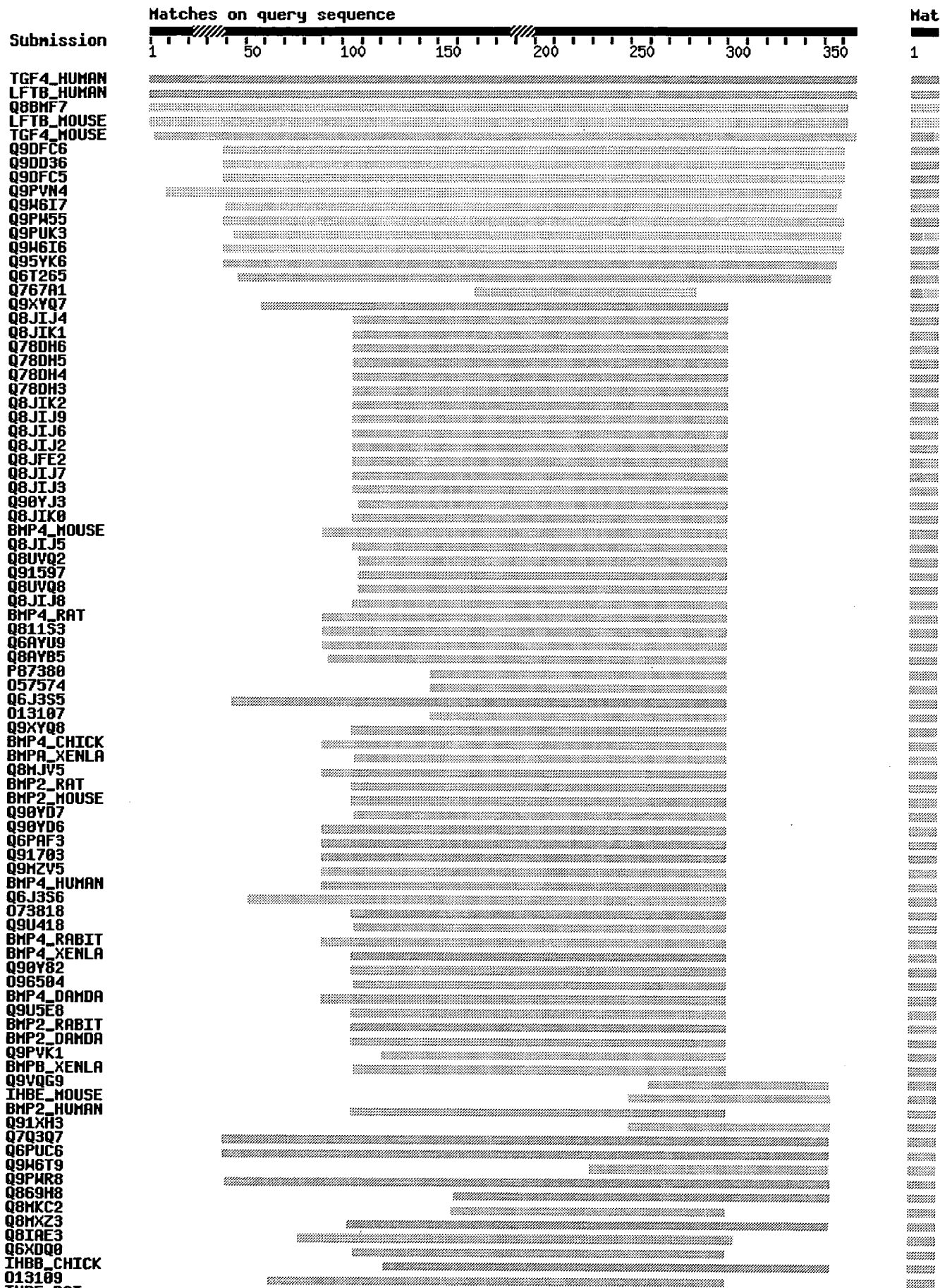
( [Help](#)) (use [ScanProsite](#) for more details about PROSITE matches)

Profile hits

Pfam hits

TGFb_propeptide

TGF_beta



Alignments

sp O00292 **Transforming growth factor beta 4 precursor (TGF-beta 4)** 366 AA
 TGF4_HUMAN **(Endometrial bleeding-associated factor) (Left-right determination factor A) (Lefty-A protein) [EBAF] [Homo sapiens (Human)]** align

Score = 684 bits (1765), Expect = 0.0
 Identities = 337/366 (92%), Positives = 337/366 (92%)

Query: 1 MWPLWLCWALWVLPLAGPGAALTXXXXXXXXXXXXXXXXXXVPVLDRADMEKLVI PAHVRAQ 60
 MWPLWLCWALWVLPLAGPGAALT VPVLDRADMEKLVI PAHVRAQ
 Sbjct: 1 MWPLWLCWALWVLPLAGPGAALTEEQLLGSLLRQLQLSEVPVLDRADMEKLVI PAHVRAQ 60

Query: 61 YVLLRRSHGDRSRGKRFSQSFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRL 120
 YVLLRRSHGDRSRGKRFSQSFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRL
 Sbjct: 61 YVLLRRSHGDRSRGKRFSQSFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRL 120

Query: 121 FQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDV 180
 FQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDV
 Sbjct: 121 FQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDV 180

Query: 181 TEAVNFWXXXXXXXXXXXXXXXXXSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTL 240
 TEAVNFW VSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTL
 Sbjct: 181 TEAVNFWQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTL 240

Query: 241 DLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300
 DLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQP
 Sbjct: 241 DLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300

Query: 301 PEALAFNWPFLGPRQCIASETASLPMIVSIKEGGRTRPQVVS LPMNRVQKSCASDGALV 360
 PEALAFNWPFLGPRQCIASETASLPMIVSIKEGGRTRPQVVS LPMNRVQKSCASDGALV
 Sbjct: 301 PEALAFNWPFLGPRQCIASETASLPMIVSIKEGGRTRPQVVS LPMNRVQKSCASDGALV 360

Query: 361 PRRLQP 366
 PRRLQP
 Sbjct: 361 PRRLQP 366

sp O75610 **Left-right determination factor B precursor (Lefty-B** 366
 LFTB_HUMAN **protein)** AA
(UNQ278/PRO317) [LEFTB] [Homo sapiens (Human)] align

Score = 654 bits (1688), Expect = 0.0
 Identities = 323/366 (88%), Positives = 328/366 (89%)

Query: 1 MWPLWLCWALWVLPLAGPGAALTXXXXXXXXXXXXXXXXXXVPVLDRADMEKLVI PAHVRAQ 60
 M PLWLCWALWVLPLA PGAALT VP LDRADME+LVIP HVRAQ
 Sbjct: 1 MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQ 60

Query: 61 YVLLRRSHGDRSRGKRFSQSFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRL 120
 YV LL+RSHGDRSRGKRFSQSFREVAGRFLA EASTHLLVFGMEQRLPPNSELVQAVLRL
 Sbjct: 61 YVALLQRSHGDRSRGKRFSQSFREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRL 120

Query: 121 FQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDV 180

```

      FQEPVPKAAALHRHGRSLSPRSA+ARVTVEWLRVRDDGNSRNTSLIDSRLVSVHESGWKAFDV
Sbjct: 121 FQEPVPKAAALHRHGRSLSPRSARARVTVEWLRVRDDGNSRNTSLIDSRLVSVHESGWKAFDV 180

Query: 181 TEAVNFWXXXXXXXXXXXXXXXXXSVQREHLGPLASGAHKLVRFAFASQGAPAGLGEPQLELHTL 240
      TEAVNFW                                VSVQREHLGPLASGAHKLVRFAFASQGAPAGLGEPQLELHTL
Sbjct: 181 TEAVNFWQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFAFASQGAPAGLGEPQLELHTL 240

Query: 241 DLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWNVLEPPGFLAYECVGTCQQP 300
      DL DYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWA+NWVLEPPGFLAYECVGTC+QP
Sbjct: 241 DLGDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWNVLEPPGFLAYECVGTCRQP 300

Query: 301 PEALAFNWPFLGPRQCIASETASLPMIVSIKEGGRTRPQVVSPLPNMRVQKCSCASDGALV 360
      PEALAF WPFLGPRQCIASET SLPIMIVSIKEGGRTRPQVVSPLPNMRVQKCSCASDGALV
Sbjct: 301 PEALAFKWPFLLGPRQCIASETDSLPMIVSIKEGGRTRPQVVSPLPNMRVQKCSCASDGALV 360

Query: 361 PRRLQP 366
      PRRLQP
Sbjct: 361 PRRLQP 366

```

```

tr Q8BMF7 Mus musculus 13 days embryo male testis cDNA, RIKEN full- 368
length enriched library, clone:6030463A22 product:LEFT-RIGHT AA
DETERMINATION FACTOR B (LEFTY-2 PROTEIN), full insert align
sequence (Endometrial bleeding associated factor) [Ebaf]
[Mus musculus (Mouse)]

```

Score = 567 bits (1461), Expect = e-160
Identities = 274/364 (75%), Positives = 299/364 (81%), Gaps = 2/364 (0%)

```

Query: 1 MWPLWLCWALWVLPLAGPGAALTXXXXXXXXXXXXXXXXXVPVLDRADMEKLVI PAHVRAQ 60
      M LWLCWALWVLPLAGPGAA+T P LD AD+E++ IP HVR+Q
Sbjct: 1 MKSLWLCWALWVLPLAGPGAAMTEEQVLSSLLQQLQLSQAPTLDSADVEEMAIP THVRSQ 60

Query: 61 YVLLRRSHGDRSRGKRFSQS FREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRL 120
      YV LL+ SH DRSRGKRFSQ+ FREVAGRFL SE STHLLVFGMEQRLPPNSELVQAVLRL
Sbjct: 61 YVALLQGSADRSRGKRFSQNFREVAGRFLMSETSTHLLVFGMEQRLPPNSELVQAVLRL 120

Query: 121 FQEPVPKAAALHRHGRSLSPSAQARVTVEWLRVRDDGNSRNTSLIDSRLVSVHESGWKAFDV 180
      FQEPVP+ AL R RLSP SA+ARVT+EWLRVR+DGSNRT+LIDSRLVS+HESGWKAFDV
Sbjct: 121 FQEPVPRTALRRFERLSPHSARARVTIEWLRVREDGNSRTALIDSRLVSIHESGWKAFDV 180

Query: 181 TEAVNFWXXXXXXXXXXXXXXXXXSVQREHLGPLASGAHKLVRFAFASQGAP--AGLGEPQLELH 238
      TEAVNFW                                VSVQREHLGP AHKLVRFA+QG P G GEPQLELH
Sbjct: 181 TEAVNFWQQLSRPRQPLLLQVSVQREHLGPGTWSAHKLVRFAAQGTPDGKGQGE PQLELH 240

Query: 239 TLDLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWNVLEPPGFLAYECVGTCQ 298
      TLDL+DYGAQG+CDPE P+TEGTRCCRQEMY+DLQGMKWA+NW+LEPPGF L YECVG+C
Sbjct: 241 TLDLKDYGAGNCDPEVPVTEGTRCCRQEMYLDLQGMKWAENWILEPPGF LTYECVGSCL 300

Query: 299 QPPEALAFNWPFLGPRQCIASETASLPMIVSIKEGGRTRPQVVSPLPNMRVQKCSCASDGA 358
      Q PE+L WPFLGPRQC+ASE SLPIMIVS+KEGGRTRPQVVSPLPNMRVQ CSCASDGA
Sbjct: 301 QLPESLTIGWPFLGPRQCVASEMTSLPMIVSVKEGGRTRPQVVSPLPNMRVQTCSCASDGA 360

Query: 359 LVPR 362
      L+PR

```

Sbjct: 361 LIPR 364

sp P57785 **Left-right determination factor B precursor (Lefty-2** 368
 LFTB_MOUSE **protein)** AA
[Leftb] [Mus musculus (Mouse)] align

Score = 565 bits (1455), Expect = e-160
 Identities = 273/364 (75%), Positives = 298/364 (81%), Gaps = 2/364 (0%)

Query: 1 MWPLWLCWALWVLPLAGPGAALTXXXXXXXXXXXXXXXXXXVPVLDRADMEKLVIPAHVRAQ 60
 M LWLCWALWVLPLAGPGAA+T P LD AD+E++ IP HVR+Q
 Sbjct: 1 MKSLWLCWALWVLPLAGPGAAMTEEQVLSSLLQQLQLSQAPTLDSDADVEEMAIPTHVRSQ 60

Query: 61 YVLLRRSHGDRSRGKRFSQSFRVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRL 120
 YV LL+ SH DRSRGKRFSQ+ REVAGRFL SE STHLLVFGMEQRLPPNSELVQAVLRL
 Sbjct: 61 YVALLQGSHADRSRGKRFSQNLREVAGRFLMSETSTHLLVFGMEQRLPPNSELVQAVLRL 120

Query: 121 FQEPVPKAAALHRHGRLSPRSAQARVTVEWLRVRDDGNSRTSLIDSRLVSVHESGWKAFDV 180
 FQEPVP+ AL R RLSP SA+ARVT+EWLRVR+DGSNRT+LIDSRLVS+HESGWKAFDV
 Sbjct: 121 FQEPVPRTALRRFERLSPHSARARVTIEWLRVREDGNSRTALIDSRLVSIHESGWKAFDV 180

Query: 181 TEAVNFWXXXXXXXXXXXXXXXXXSVQREHLGPLASGAHKLVRFASQGAP--AGLGEPQLELH 238
 TEAVNFW VSVQREHLGP AHKLVRF+QG P G GEPQLELH
 Sbjct: 181 TEAVNFWQQLSRPRQPLLLQVSVQREHLGPGTWSAHKLVRF+AAQGTDPGKGQGEPELH 240

Query: 239 TLDLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQ 298
 TLDL+DYGAQG+CDPE P+TEGTRCCRQEMY+DLQGMKWA+NW+LEPPGF L YECVG+C
 Sbjct: 241 TLDLKDYGAQGNCDPEVPVTEGTRCCRQEMYLDLQGMKWAENWILEPPGFLTYECVGSCL 300

Query: 299 QPPEALAFNWPFLGPRQCIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKSCASDGA 358
 Q PE+L WPFLGPRQC+ASE SLPIMVS+KEGGRTRPQVVSLPNMRVQ CSCASDGA
 Sbjct: 301 QLPESLTIGWPFLGPRQCVASEMTSLPMIVSVKEGGRTRPQVVSLPNMRVQTCSCASDGA 360

Query: 359 LVPR 362
 L+PR
 Sbjct: 361 LIPR 364

sp Q64280 **Transforming growth factor beta 4 precursor (TGF-beta 4)** 368
 TGF4_MOUSE **(Lefty** AA
protein) (Lefty-1 protein) (STRA3 protein) [Ebaf] [Mus align
musculus (Mouse)]

Score = 556 bits (1432), Expect = e-157
 Identities = 271/365 (74%), Positives = 295/365 (80%), Gaps = 2/365 (0%)

Query: 4 LWLCWALWVLPLAGPGAALTXXXXXXXXXXXXXXXXXXVPVLDRADMEKLVIPAHVRAQYVV 63
 LWLCWALW L L ALT PVLD+AD+E +VIP+HVR QYV
 Sbjct: 4 LWLCWALWALSLSLREALTGEQILGSLQQLQLDQPPVLDKADVEGMVIPSHVRTQYVA 63

Query: 64 LLRRSHGDRSRGKRFSQSFRVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRLRFQE 123
 LL+ SH RSRGKRFSQ+ REVAGRFL SE STHLLVFGMEQRLPPNSELVQAVLRLRFQE
 Sbjct: 64 LLQHSASRSRGKRFSQNLREVAGRFLVSETSTHLLVFGMEQRLPPNSELVQAVLRLRFQE 123

Query: 124 PVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEA 183
PVP+ AL R RLSP SA+ARVT+EWLR RDDGSNRT+LIDSRLVS+HESGWKAFDVTEA
Sbjct: 124 PVPRTALRRQKRLSPHSARARVTIEWLRFRDDGSNRTALIDSRLVSIHESGWKAFDVTEA 183

Query: 184 VNFVXXXXXXXXXXXXXXXXXSVQREHLGPLASGAHKLVRFAAQGAP--AGLGEPQLELHTLD 241
VNFV VSVQREHLGP +HKLVRFA+QG P G GEPQLELHTLD
Sbjct: 184 VNFVQQLSRPRQPLLLQVSVQREHLGPGTWSSHKLVRFAAQGTPDGKGQGEPOLELHTLD 243

Query: 242 LRDYGAQGDCEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCCQPP 301
L+DYGAQG+CDPEAP+TEGTRCCRQEMY+DLQGMKWA+NW+LEPPGFL YECVG+C Q P
Sbjct: 244 LKDYGAQGNCDPEAPVTEGTRCCRQEMYLDLQGMKWAENWVLEPPGFLTYECVGSCLQLP 303

Query: 302 EALAFNWPFLGPRQCIASETASLPMIVSIKEGGTRTPQVVSLPNMRVQKSCASD GALVP 361
E+L WPFLGPRQC+ASE SLPMIVS+KEGGTRTPQVVSLPNMRVQ CSCASD GAL+P
Sbjct: 304 ESLTSRWPFLGPRQCVASEMTSLPMIVSVKEGGTRTPQVVSLPNMRVQTCASD GALIP 363

Query: 362 RRLQP 366
RRLQP
Sbjct: 364 RRLQP 368

tr Q9DFC6 **TGF-beta family member lefty-A [Xenopus laevis (African clawed frog)]** 366 AA

align

Score = 232 bits (592), Expect = 7e-60

Identities = 126/330 (38%), Positives = 193/330 (58%), Gaps = 16/330 (4%)

Query: 40 VPVLDRADMEKLVIPAHVRAQYVLLRRSHGDRSRGK-----RFSQSFREVAGRFLA 91
VP L++ D+E LVIP H++A+Y+ +L SH +R R R +++G L
Sbjct: 43 VPKLEKRDVENLVIPRHIQAKYMSMLH-SHRERKRRSLPSLAGILRGISGNADISGEILY 101

Query: 92 SEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPAALHRHGRLSPRSAQARVTVEWLR 151
S++S +VFGME R+P NSE+ A L+LF++P PK R + ARV+V ++
Sbjct: 102 SDSSKQTMVFGMESRIPENSEVTMAELKLFKKP-PKIMNVPERFRHRPVSNA RVSVYYVE 160

Query: 152 VRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFVXXXXXXXXXXXXXXXXXSVQREHLGPL 211
+ DG+NRTSL+DSRLV + ESGW++FDVT+AV++W + V E G
Sbjct: 161 ILKDGTNRTSLVDSRLVPIMESGWSFDVTQAVHYW-MKSGGHSSMHLEIHVDGERHGSH 219

Query: 212 ASGAHKLVRFAAQG-APAGLGEPQLELHTLDLRDYGAQGDCEAPMTEGTRCCRQEMYI 270
AS K+VRF +Q + LG+P+L L TL+L ++GA+GDC + CCR+E +I
Sbjct: 220 ASEMAKMVRFTTQSPSDNSLGKPELVLFNLDEHGARGDCSASGAKKDNI-CCREYFI 278

Query: 271 DLQGMKWAENWVLEPPGFLAYECVGTCCQPPPEALAFNWPFLGPRQCIASETASLPMIVSI 330
+ + + W + W++EP G+ A+ C G+C+QP L+ ++ G R C E+A LP++ +
Sbjct: 279 NFRELTWTQYWIIEPAGYNAFRACAGSCKQPKYPLSHHY---GERMCAVVESAPLPV MYLV 335

Query: 331 KEGGRTRTPQVVSLPNMRVQKSCASD GALV 360
K+G T +V PNM V+KC C D +
Sbjct: 336 KKG DYTEIEVAEFPNMIVEKCGCTMDNIAI 365

tr Q9DD36 **Xantivin (Lefty-related factor Xatv) [Xantivin] [Xenopus laevis]** 367 AA

(African clawed frog)]

align

Score = 229 bits (583), Expect = 8e-59

Identities = 128/337 (37%), Positives = 190/337 (55%), Gaps = 29/337 (8%)

Query: 40 VPVLDRADMEKLVIPAHVRAQYVVLLRRSHGDRSRGKRFSQSFR-----EVAGR 89
VP L++ D+E LVIP H++A+Y+ +L H R R KR S +++G

Sbjct: 43 VPKLEKRDVENLVIPGHIQAKYMSML---HNHRERKKRSLPSLAGILRGISGNADISGEI 99

Query: 90 LASEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP-----VPKAALHRHGRSLSPRSAQAR 144
L S++S LVFGME R+P NSE+ A L+LF++P VP+ HR AR

Sbjct: 100 LYSOSSKQSLVFGMESRIPENSEVTMAELKLFKKPPKIMNVPERRFHRPVN-----NAR 153

Query: 145 VTVEWLRVRDDGNSRTSLIDSRLVSVHESGWKAFDVTAVNFWXXXXXXXXXXXXXVSQ 204
V+V ++ + DG+NRTSL+DSRLV + ESGW++FDVT+AV++W + V

Sbjct: 154 VSVYYVEILKDGTNRTSLVDSRLVPIMESGWSFDVTQAVHYW-MRSGGQSSMHLEIHVD 212

Query: 205 REHLGPIASGAHKLVRFASQG-APAGLGEPQLELHTLDLRDYGAQGDCDPEAPMTEGTRC 263
E G AS K+VRF +Q + LG+P+L L TL+L + G +GDC + C

Sbjct: 213 GERHGSHASEMAKMVRFTTQSPSDNSLGKPELVLFNLNEQGTGDCSASGAKKDNI-C 271

Query: 264 CRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCCQPPEALAFNWPFLGPRQCIASETAS 323
CR+E +I+ + + W + W++EP G+ A+ C G+C+QP L+ G R C E+A

Sbjct: 272 CREEYFINFRELTTWTQYWIIEPAGYNAFRCTGSCKQPKYPLSHY--HYGQRTCAVVESEAP 329

Query: 324 LPMIVSIKEGGRTRPQVVSPLNMRVQKCSASDGLV 360
LP++ +K+G T +V PNM V+KC C D +

Sbjct: 330 LPVMYLVKKGDYTEIEVAEFPNMIVEKCGCTMDNIAI 366

tr Q9DFC5 TGF-beta family member lefty-B [Xenopus laevis (African clawed 367 AA
frog)]

align

Score = 228 bits (582), Expect = 1e-58

Identities = 128/337 (37%), Positives = 190/337 (55%), Gaps = 29/337 (8%)

Query: 40 VPVLDRADMEKLVIPAHVRAQYVVLLRRSHGDRSRGKRFSQSFR-----EVAGR 89
VP L++ D+E LVIP H++A+Y+ +L H R R KR S +++G

Sbjct: 43 VPKLEKRDVENLVIPRHIIQAKYMSML---HNHRERKKRSLPSLAGILRGISGNADISGEI 99

Query: 90 LASEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP-----VPKAALHRHGRSLSPRSAQAR 144
L S++S LVFGME R+P NSE+ A L+LF++P VP+ HR AR

Sbjct: 100 LYSOSSKQSLVFGMESRIPENSEVTMAELKLFKKPPKIMNVPERRFHRPVN-----NAR 153

Query: 145 VTVEWLRVRDDGNSRTSLIDSRLVSVHESGWKAFDVTAVNFWXXXXXXXXXXXXXVSQ 204
V+V ++ + DG+NRTSL+DSRLV + ESGW++FDVT+AV++W + V

Sbjct: 154 VSVYYVEILKDGTNRTSLVDSRLVPIMESGWSFDVTQAVHYW-MRSGGQSSMHLEIHVD 212

Query: 205 REHLGPIASGAHKLVRFASQG-APAGLGEPQLELHTLDLRDYGAQGDCDPEAPMTEGTRC 263
E G AS K+VRF +Q + LG+P+L L TL+L + G +GDC + C

Sbjct: 213 GERHGSHASEMAKMVRFTTQSPSDNSLGKPELVLFNLNEQGTGDCSASGAKKDNI-C 271

Query: 264 CRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCCQPPEALAFNWPFLGPRQCIASETAS 323
CR+E +I+ + + W + W++EP G+ A+ C G+C+QP L+ G R C E+A

Sbjct: 272 CREEYFINFRELTTWTQYWIIEPAGYNAFRCTGSCKQPKYPLSHY--HYGQRTCAVVESEAP 329

Query: 324 LPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALV 360
LP++ +K+G T +V PNM V+KC C D +
Sbjct: 330 LPVMYLVKKGDYTEIEVAEFPMIIVEKCGCTMDNIAI 366

tr Q9PVN4 Lefty [Gallus gallus (Chicken)] 362 AA
align

Score = 226 bits (575), Expect = 7e-58
Identities = 131/352 (37%), Positives = 187/352 (52%), Gaps = 8/352 (2%)

Query: 10 LWVLPLAGPGAALTXXXXXXXXXXXXXXXXXVPVLDRADMEKLVIPAHVRAQYVVLLRRSH 69
L+VL L A T VP L + D+ LVIP HV+ +Y+ +L+R
Sbjct: 9 LYVLCIVAMACAFTEGFEKVMKQLGLSEVPKLHKRDLVDLVIPEHVKNKYISMLKRHR 68

Query: 70 GDRSRGKRFSQSFREVAGR--FLASEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPK 127
G R + + + G S+ +F ME R+P NSE+ A L+LF++P+ +
Sbjct: 69 GKRRASPSLASILQGIPEGNAEVFYSDFMRQNFIFDMEGRIPKNSEVTMAELKLFKKPLDR 128

Query: 128 AALHRHGRLSPRSAQARVTVEWLVRDGSNRTSLIDSRLVSVHESGWKAFDVTAVNFW 187
L P S ARV++ W++ + DG+NRTSLIDSRLV + ESGWK FDVT+AV++W
Sbjct: 129 VNLPARQPHRPVS-NARVSIYWVQRQHDGTNRTSLIDSRLVPIRESGWKNFDVTQAVHYW 187

Query: 188 XXXXXXXXXXXXXXXXSVQREHLGLASGAHKLVRFASQGA-PAGLGEPQLELHTLDRDYG 246
V ++ E + A+ K VRF SQ A +G P+L L+TLDL DYG
Sbjct: 188 -LRNKRQEPMLQVWIEGERVASIAAEVAKSVRFTSQDAGDRAVGRPELVLYTLDLEDYG 246

Query: 247 AQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAQNVLEPPGFLAYECVGTCCQPPEALAF 306
GDC + T CCRQ+ YI+ + + W + WV+EP G+ AY C G C Q P L
Sbjct: 247 GPGDCKDGVQAGKST-CCRQKHYNFRELSTQYVWIEPAGYQAYSCRGGLQLPGPLQL 305

Query: 307 NWPFLGPRQCIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGA 358
W R C +E++ LP++ ++ G T + PNM ++KCSC +DGA
Sbjct: 306 -WGG-RERACAVAESSPLPIMYLVRGNHTEIEATEFPNMIIEKCSCMADGA 355

tr Q9W6I7 Signaling molecule lefty2 [lft2] [Brachydanio rerio] 362
(Zebrafish) AA
(Danio rerio) align

Score = 219 bits (559), Expect = 5e-56
Identities = 121/330 (36%), Positives = 183/330 (54%), Gaps = 25/330 (7%)

Query: 41 PVLDRADMEKLVIPAHVRAQYVVLLRRSHGDRSRGK-----RFSQSFREVAGRFLASE 93
P + + D+E LV+PAH++++Y+ +L+ H R R R ++ G S+
Sbjct: 39 PRIQKRDLENLVPAHIKSKYLSMLKLHHQRRRSLPSLAGILRGIHGNADITGEIKYSD 98

Query: 94 ASTHLLVFGMEQRLPPNSELVQAVLRLFQEPV--PKAALHRHGRLSPRSAQARVTVEWL 151
+ LVF ME RL N+E+ A L+LFQ P RH R ARV++ W+
Sbjct: 99 TTRQRLVFDMEARLQENTEVMAELKLFQTAAQSPSKPERRHHR---PINHARVSIYWVE 155

Query: 152 VRDDGSNRTSLIDSRLVSVHESGWKAFDVTAVNFWXXXXXXXXXXXXXSVQREHLGPL 211
V ++GSNRTSL+DSRLV +HESGW++FDVT+A+++W V + E G
Sbjct: 156 VLENGSNRTSLLDLRLVPIHESGWRSFDVTQAIHYW-SKSQKKAPLHLEVWTEGERPGSY 214

Query: 212 ASGAHKLVRFA SQGAPAG-----LGEPQLELHTLDLRDYGAQGDCDPEAPMTEGTRCCRQ 266
A+ K VRFA+Q +G P+L L+TLDL +YG+QG+C+ ++CCR+
Sbjct: 215 AAEMAKRVRFATQDPKENTLEKDMGAPELVLYTLDLDEYGSQGNCS--PNSSKCCRE 271

Query: 267 EMYIDLQGMKWAKNWVLEPPGFLAYECVGTCCQPPEALAFNWPFLGPRQCIASETASLPM 326
E +I+ + + W + W++EP G+ A+ C G C+QP + G R C E+A LPM
Sbjct: 272 EHFINFRELTTWTQYWIIEPAGYQAFRCAGGCKQPKR----GFYGYGORTCAVMESAPLPM 327

Query: 327 IVSIKEGGRTRPQVVSLPNMRVQKCSASD 356
+ +K+G T +V PNM V+KC C+ D
Sbjct: 328 MYLVKKGDYTEIEVAEFPNMIVEKCGCSMD 357

tr Q9PW55 Antivin [lft1] [Brachydanio rerio (Zebrafish) (Danio rerio)] 358 AA

align

Score = 219 bits (559), Expect = 5e-56

Identities = 115/329 (34%), Positives = 185/329 (55%), Gaps = 18/329 (5%)

Query: 40 VPVLDRADMEKLVIPAHVRAQYVVLRRSHGDRSRGK-----RFSQSFREVAGRFLAS 92
+P + + D+E LVIP HV+ +Y+ +L+ H + R R +++G F+ S
Sbjct: 39 IPQIHKRDLENLVIPTHVKNKYISMLKLHHSRKRRSLPSLAGILRGIPGNADISGEFVYS 98

Query: 93 EASTHLLVFGMEQRLPPNSELVQAVLRLRFQEPVPKAAALHRHGRSLSPRQAQARVTVEWLRV 152
+ + +VF M R+P NSE+ A L+L+++ K ++ P + ARV++ W+
Sbjct: 99 DTTQRQVVFEMTSRIPENSEVTMAELKLYKKAPHKRSIPERKGRHPVN-NARVSIYWVEP 157

Query: 153 RDDGSNRTSLIDSRLVSVHESGWKAFDVTAVNFVXXXXXXXXXXXXXSVQREHLGPIA 212
+ DGSNRTSL+DSRL+ +HE+GWK+FDVT+AV +W V ++ E G A
Sbjct: 158 QKDGSNRTSLVDSRLIPIHETGWKSFVDTQAVQYW-SRSRMEMPMHLEVWIEGERPGSYA 216

Query: 213 SGAHKLVRFA SQGAPAG-LGEPQLELHTLDLRDYGAQGDCDPEAPMTEGTRCCRQEMYID 271
+ K V F +Q LG+P+L L+TL+L ++G+ GDC+ + CCR++ +I+
Sbjct: 217 AEMAKCVHFTTQDPDDNTLGKPELVLYTLNLEEFSGSDCENN---KDREMCCREQYFIN 273

Query: 272 LQGMKWAKNWVLEPPGFLAYECVGTCCQPPEALAFNWPFLGPRQCIASETASLPMIVSIK 331
+ + W + W++EP G+ A+ C G C+QP + G R+C E+A LPM+ +K
Sbjct: 274 FRALTWTQYWIIEPSGYQAFRCGGCRQPKRNYGY-----GERKCAVVESAPLPMYLVK 328

Query: 332 EGGRTTRPQVVSLPNMRVQKCSASD GALV 360
+G T +V PNM V+KC CA D V
Sbjct: 329 KGDYTEIEVAEFPNMIVEKCGCAMDNISV 357

tr Q9PUK3 LEFTY-1 protein (Fragment) [LEFTY-1] [Gallus gallus (Chicken)] 320 AA

o

align

Score = 218 bits (556), Expect = 1e-55

Identities = 122/317 (38%), Positives = 177/317 (55%), Gaps = 8/317 (2%)

Query: 45 RADMEKLVIPAHVRAQYVVLRRSHGDRSRGKRFSQSFREVAGR--FLASEASTHLLVFG 102
+ D+ LVIP HV+ +Y+ +L+R G R + + + G S+ +F
Sbjct: 2 KRDLVDLVIPEHVKNKYISMLKRHRGKRRASPSLASILQGIPGNAEVFYSDPMRQNFIFD 61

Query: 103 MEQRLPPNSELVQAVLRLRFQEPVPKAAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSL 162
 ME R+P NSE+ A L+LF++P+ + L P S ARV++ W++ + DG+NRTSL
 Sbjct: 62 MEGRIKPNSEVTMAELKLFKKPLDRVNLPARQPHRPVS-NARVSIYWVQRQHDGTNRTSL 120

Query: 163 IDSRLVSVHESGWKAFDVTAVNFWXXXXXXXXXXXXXSVQREHLGPLASGAHKLVRFA 222
 IDSRLV + ESGWK FDVT+AV++W V ++ E + A+ K VRF
 Sbjct: 121 IDSRLVPIRESGWKNFDVTQAVHYW-LRNKRQEPMLVQVWIEGERVASIAAEVAKSVRFT 179

Query: 223 SQGA-PAGLGEPQLELHTLDRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNW 281
 SQ A +G P+L L+TLDL DY GDC + T CCRQ+ YI+ + + W + W
 Sbjct: 180 SQDAGDRAVGRPELVLYTLTLDLEDYGGPGDCKDGVQAGKST-CCRQKHYINFRELSWTQYW 238

Query: 282 VLEPPGFLAYECVGTCCQPPEALAFNWPFLGPRQCIASETASLPMIVSIKEGGTRPQV 341
 V+EP G+ AY C G C Q P L W R C +E++ LP++ ++ G T +
 Sbjct: 239 VIEPAGYQAYSCRGGCLQLPGPLQL-WGG-RERACAVAESSPLPIMYLVRRGNHTEIEAT 296

Query: 342 SLPNMRVQKCSASDGA 358
 PNM ++KCSC +DGA
 Sbjct: 297 EFPNMIIKCSMADGA 313

tr Q9W6I6 **Signaling molecule lefty1 [lft1] [Brachydanio rerio** 358
(Zebrafish) AA
(Danio rerio)] align

Score = 217 bits (552), Expect = 3e-55
 Identities = 114/329 (34%), Positives = 185/329 (55%), Gaps = 18/329 (5%)

Query: 40 VPVLDRADMEKLVIPAHVRAQYVVLLRRSHGDRSRGK-----RFSQSFREAVAGRFLAS 92
 +P + + D+E LVIP +V+ +Y+ +L+ H + R R +++G F+ S
 Sbjct: 39 IPQIHKRDLENLVIPTNVKNKYISMLKLHHSRKRSLPSLAGILRGIPGNADISGEFVYS 98

Query: 93 EASTHLLVFGMEQRLPPNSELVQAVLRLRFQEPVPKAAALHRHGRLSPRSAQARVTVEWLRV 152
 + + +VF M R+P NSE+ A L+L+++ K ++ P + ARV++ W+
 Sbjct: 99 DTTRQRVVFEMTSRIPENSEVTMAELKLYKKAPHKRSIPERKGRHPVN-NARVSIYWVEP 157

Query: 153 RDDGSNRTSLIDSRLVSVHESGWKAFDVTAVNFWXXXXXXXXXXXXXSVQREHLGPLA 212
 + DGSNRTSL+DSRL+ +HE+GWK+FDVT+AV +W V ++ E G A
 Sbjct: 158 QKDGSNRTSLVDSRLIPIHETGWKSFVDVTQAVQYW-SRSRMEMPMHLEVWIEGERPGSYA 216

Query: 213 SGAHKLVRFASQGAPAG-LGEPQLELHTLDRDYGAQGDCDPEAPMTEGTRCCRQEMYID 271
 + K V F +Q LG+P+L L+TL+L ++G+ GDC+ + CCR++ +I+
 Sbjct: 217 AEMAKCVHFTTQDPDDNTLGKPELVLYTLNLEEFSSGDCENN---KDREMCCREQYFIN 273

Query: 272 LQGMKWAKNWVLEPPGFLAYECVGTCCQPPEALAFNWPFLGPRQCIASETASLPMIVSIK 331
 + + W + W++EP G+ A+ C G C+QP + G R+C E+A LPM+ +K
 Sbjct: 274 FRALTWTQYWIIEPSGYQAFRCKGGCRQPKRNYGY-----GERKCAVVESAPLPMYLVK 328

Query: 332 EGGTRPQVVS LPMNRVQKCSASDGA 360
 +G T +V PNM V+KC CA D V
 Sbjct: 329 KGDYTEIEVAEFPNMIVEKCGCAMDNISV 357

tr Q95YK6 **Lefty/antivin related protein [Cs-lfan] [Ciona** 372 AA

savignyi]

align

Score = 145 bits (366), Expect = 1e-33

Identities = 107/348 (30%), Positives = 160/348 (45%), Gaps = 43/348 (12%)

Query: 40 VPVLDRADMEKLVIPAHVRAQYVLLRR-SHGDRSRGKRFSQS-FREV-----AGRFLA 91
VP ++ +VIP R +Y ++ + + +R+R Q FR V G +
Sbjct: 32 VPRFTHNEVRNVVIPDETTRKYERMVEKMTKLERNRRSSSLQDLFRSVHKKTGIEGDVIY 91

Query: 92 SEASTHLLVFGMEQRLPFPNSELVQAVLRLFQEPVPAALHRHGRL----- 136
S+ L F ME RLP + + A LRLF++ L H R+
Sbjct: 92 SDTFREELKFDMEGRLPDDYMISMAELRLFKK-----LPNHNRLSRLRTPSGNRNDVQ 145

Query: 137 --SPRSAQ-----ARVTVEWLRVRDDGNSRSLIDSLVSVHESGWKAFDVTAVNFWXX 189
S R Q ARV++ DG T L+DSRL+ V+ SGW FDVT A+ W
Sbjct: 146 LSSARGRQQVIRNARVSIHLSLPLPDGGAVTELVDLSRLILVNGSGWHTFDVTSAIRKWRR 205

Query: 190 XXXXXXXXXXXXSVQREHLGPLASGAHKLVRFASQG-APAGLGEPQLELHTLDRDYGAQ 248
+ VQ G A+ +L+RF Q A P+L ++T + ++
Sbjct: 206 HPVRYMTITLELKVQSSSPGAAAELARLIRFTGQRVALDSPRRPELVVYT-NAKEPART 264

Query: 249 GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQOPPEALAFNW 308
DC + +CCR+ +++ + KW+K+W+LEP GF AY C G C+ , +
Sbjct: 265 SDCSSSRHNRQH-KCCRENRFVNFRETQWSKHWILEPAGFNAYHCAGGCRSDRRRNSKG- 322

Query: 309 PFLGPRQCIASETASLPMIVSIKEGGRTRPQVVS LPMNRVQKSCASD 356
PR C A+ET SLP++ +K+GG +V PNM ++KSCA D
Sbjct: 323 ---APRSCSATETNSLPIMYLKKGGAHVEVSEFPNMVIEKSCALD 367

tr Q6T265 Antivin/lefty [Paracentrotus lividus (Common sea urchin)] 404 AAalign

Score = 103 bits (256), Expect = 6e-21

Identities = 89/359 (24%), Positives = 138/359 (37%), Gaps = 60/359 (16%)

Query: 47 DMEKLVIPAHVRAQYVLLRRSHGDRSRGKRFSQSFREVAGRFLASEASTHLLVFGMEQR 106
D L +P H+R QY + R+ R+ + E+ G +E + L F +
Sbjct: 52 DASTLTPDHLRFQYESMHRQHRVRRAYITKGIHKNEEIYGEVSYTERNRQLFTFDISS- 110

Query: 107 LPPNSELVQAVLRLFQE-----PVPKAALHRHGRLSPRSAQARVT----- 146
+P SE++ A L+++E P + H H + S + V
Sbjct: 111 IPEGSEVIMAE LKVYKERPNHSIFKPEGEEGEAPHSNNHDHVSALVSIKQLVDQEVDM 170

Query: 147 VEWLRVRDDGNSR-----TSLIDSLVSVHESGWKAFDVTAVNFWXXXXXXXXXXXXXV 201
E + D+ N+ T ID R +++ +GWK FDVT + W
Sbjct: 171 AEPADLADEVVNQHDGMDTITIDQREMTLKGAGWKVFDVTNTIQTWVADSDSNLGVAL-- 228

Query: 202 SVQREHLGPLASGAHKL-----VRFASQGAPAGLGEPQLELHTLDRDYGAQGDCDPEAP 256
H+ P+ G H + FA+ P P + A +P
Sbjct: 229 -----HIDPIEGGHHAQQVVDDEMVFATDFFPETPDSPDSRPVLVIYTTKYAPASDEPNEC 283

Query: 257 MTEGT---RCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQOPPEAL---AFNWPF 310
EG RCCR+ Y+D + + W W++EP GF A++C G C P F PF
Sbjct: 284 RYEGEEHRCRRRRKYVDFRDLSWTSRWIIEPAGFEAFDCYGPCHNPRSRHIRDVFRLLPF 343

Query: 311 LGP-----RQCIASETASLPMI-VSIKEGGRTRPQVVSLPNMRVQKCSC 353
G R C S ++SLPM+ +S G +V +PNM V+ C C
Sbjct: 344 FGASSSGSSIFGAGSGGHRCTCGVSRSSSLPMYLSETPSGTVELKVEEIPNMIVEDCGC 402

tr Q767A1 **Signaling molecule lefty1 (Fragment) [lefty1] [Oryzias latipes 112 AA**
(Medaka fish) (Japanese ricefish)] align

Score = 84.0 bits (206), Expect = 4e-15
Identities = 41/115 (35%), Positives = 66/115 (56%), Gaps = 5/115 (4%)

Query: 170 VHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSQREHLGPLASGAHKLVRFASQGAPAG 229
+HE+GWK+FDVT+AV++W V ++ E G A+ K VRF +Q
Sbjct: 2 IHETGWKSFDVTQAVHYW-SKTQOKTPMHLEVWIEGERPGSYAAEVAKSVRFTTQEOTEH 60
Query: 230 L-GEPLQELHTLRLDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVL 283
G+P+L L+TL+L +YG++GDCD CCR++ +ID + + W + W++
Sbjct: 61 TSGKPELVLYTLNLEEYGSRGDCD---VYQSKDTCCREQYFIDFRALTWTQYWII 112

tr Q9XYQ7 **Bone morphogenetic protein BMP2/4 [BMP2/4] [Lytechinus 417**
variegatus AA
(Sea urchin)] align

Score = 69.3 bits (168), Expect = 1e-10
Identities = 70/280 (25%), Positives = 110/280 (39%), Gaps = 47/280 (16%)

Query: 60 QYVLLRRSHGDRSRGKRFSQSF-----REVAGRFLASEASTHLLVFGME 104
QY++ L RSH + G F E AG+ L +E H ++F +
Sbjct: 81 QYMDLYRSHTHQDGISMHFDFDHLSTGTANTIRSYHHEDAGQVLPTEHHRHTVIFNIS 140
Query: 105 QRLPPNSELVQAVLRLRFQEPVPKAAALHRHGRLSPRSA-----QARVTVEWLRVRDDGSN 158
+P L A LRLF++ + + + + L R + R+ V + ++ N
Sbjct: 141 T-MPAEEVLTMALRLFRKDLEEHSIAKRHALDDRKSLEPIHYMQRINVFHI-LKPVARN 198
Query: 159 RTS---LIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSQREHLGPLASGA 215
R + LID+RLV V S W++FDV AV W + R P
Sbjct: 199 RDTIKRLIDTRLVDVRNSSWESFDVRPAVTSWVEVPEKNHGLEIELIDSRGRPSP---N 254
Query: 216 HKLVRFASQGAPAGLGEPLQELHTL-----DLRDYGAQGDCDPEAPMTEGTR----- 262
H VR + P+ + E Q E + Y G +P + G +
Sbjct: 255 HHHVRVTREADPSKVQELQNEEDERWFQTRPQIVTYSDDGR-TKRSPSSRGRKRKGKRLK 313
Query: 263 --CCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
C R +Y+D + W +W++ P G+ AY C G C P
Sbjct: 314 ANCRRHPLYVDFSDVHW-NDWIVAPAGYQAYYCHGECPPF 352

tr Q8JIJ4 **Bmp4 protein [Bmp4] [Steatocranus casuarius (lionhead 403**
cichlid)] align

Score = 67.4 bits (163), Expect = 4e-10
Identities = 60/205 (29%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLRFQEPVPKAAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
+P + L A LRL++ + +A +S A R+ V E L+ G T L+DS
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEV LKAPRPGQLITQLLDS 201

Query: 166 RLVS VHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREHLGPLASGAHKLVRFASQG 225
RLV + S W++FDV+ AV W V V + P G H + +
Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP-----EAPMTEGTR----CCRQEMYIDLQGM 275
P GE +L L L +G G P +P G + C R +Y+D +
Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSRQRGRKRNRCRRHALYVDFSDV 315

Query: 276 KWAKNWWLEPPGFLAYECVGTCCQP 300
W +W++ PPG+ AY C G C P
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECFPF 339

tr Q8JIK1 **Bmp4 protein [Bmp4] [Ctenochromis horei]** 403 AA
align

Score = 66.6 bits (161), Expect = 7e-10
Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLRFQEPVPKAAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
+P + L A LRL++ + +A +S A R+ V E L+ G T L+D+
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEV LKAPRPGQLITQLLDT 201

Query: 166 RLVS VHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREHLGPLASGAHKLVRFASQG 225
RLV + S W++FDV+ AV W V V + P G H + +
Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP-----EAPMTEGTR----CCRQEMYIDLQGM 275
P GE +L L L +G G P +P G + C R +Y+D +
Sbjct: 260 EP---GEDWKQLRPL-LVTFGHDGKGHPLTRRTKRSRQRGRKRNRCRRHALYVDFSDV 315

Query: 276 KWAKNWWLEPPGFLAYECVGTCCQP 300
W +W++ PPG+ AY C G C P
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECFPF 339

tr Q78DH6 **Bmp4 protein [Bmp4] [Gnathochromis permaxillaris]** 403 AA
align

Score = 66.2 bits (160), Expect = 9e-10
Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLRFQEPVPKAAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
+P + L A LRL++ + +A +S A R+ V E L+ G T L+D+
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEV LKAPRPGQLITQLLDT 201

Query: 166 RLVS VHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREHLGPLASGAHKLVRFASQG 225
RLV + S W++FDV+ AV W V V + P G H + +

Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP-----EAPMTEGTR----CCRQEMYIDLQGM 275
P GE +L L L +G G P +P G + C R +Y+D +

Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSRQRGRKRNRCRRHALYVDFSDV 315

Query: 276 KWAKNWWLEPPGFLAYECVGTCQQP 300
W +W++ PPG+ AY C G C P

Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECPPF 339

tr Q78DH5 **Bmp4 protein [Bmp4] [Haplotaxodon microlepis]** 403 AA
align

Score = 66.2 bits (160), Expect = 9e-10
Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLRFQEPVPKAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
+P + L A LRL++ + +A +S A R+ V E L+ G T L+D+

Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVEVLKAPRPGQLITQLLDT 201

Query: 166 RLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREHLGPLASGAHKLVRFASQG 225
RLV + S W++FDV+ AV W V V + P G H + +

Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP-----EAPMTEGTR----CCRQEMYIDLQGM 275
P GE +L L L +G G P +P G + C R +Y+D +

Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSRQRGRKRNRCRRHALYVDFSDV 315

Query: 276 KWAKNWWLEPPGFLAYECVGTCQQP 300
W +W++ PPG+ AY C G C P

Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECPPF 339

tr Q78DH4 **Bmp4 protein [Bmp4] [Ophthalmotilapia nasuta]** 403 AA
align

Score = 66.2 bits (160), Expect = 9e-10
Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLRFQEPVPKAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
+P + L A LRL++ + +A +S A R+ V E L+ G T L+D+

Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVEVLKAPRPGQLITQLLDT 201

Query: 166 RLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREHLGPLASGAHKLVRFASQG 225
RLV + S W++FDV+ AV W V V + P G H + +

Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP-----EAPMTEGTR----CCRQEMYIDLQGM 275
P GE +L L L +G G P +P G + C R +Y+D +

Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSRQRGRKRNRCRRHALYVDFSDV 315

Query: 276 KWAKNWWLEPPGFLAYECVGTCQQP 300
W +W++ PPG+ AY C G C P

Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECPPF 339

tr Q78DH3 **Bmp4 protein [Bmp4] [Tanganicodus irsacae (Spotfin goby cichlid)]** 403
AA
align

Score = 66.2 bits (160), Expect = 9e-10
Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLRFQEPVPKAAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
+P + L A LRL++ + +A +S A R+ V E L+ G T L+D+
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEV LKAPRPGQLITQLLDT 201

Query: 166 RLVS VHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREHLGPLASGAHKLVRFASQG 225
RLV + S W++FDV+ AV W V V + P G H + +
Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP-----EAPMTEGTR----CCRQEMYIDLQGM 275
P GE +L L L +G G P +P G + C R +Y+D +
Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSRQGRKRNRNCRRHALYVDFSDV 315

Query: 276 KWAKNWWLEPPGFLAYECVGTCQQP 300
W +W++ PPG+ AY C G C P
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECFP 339

tr Q8JIK2 **Bmp4 protein [Bmp4] [Astatoreochromis alluaudi (Alluaud's haplo)]** 403
AA
align

Score = 66.2 bits (160), Expect = 9e-10
Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLRFQEPVPKAAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
+P + L A LRL++ + +A +S A R+ V E L+ G T L+D+
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEV LKAPRPGQLITQLLDT 201

Query: 166 RLVS VHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREHLGPLASGAHKLVRFASQG 225
RLV + S W++FDV+ AV W V V + P G H + +
Sbjct: 202 RLVGHNVSRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP-----EAPMTEGTR----CCRQEMYIDLQGM 275
P GE +L L L +G G P +P G + C R +Y+D +
Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSRQGRKRNRNCRRHALYVDFSDV 315

Query: 276 KWAKNWWLEPPGFLAYECVGTCQQP 300
W +W++ PPG+ AY C G C P
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECFP 339

tr Q8JIJ9 **Bmp4 protein [Bmp4] [Haplochromis burtoni (Burton's mouthbrooder)]** 403
AA
align

Score = 66.2 bits (160), Expect = 9e-10
Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLRFQEPVPKAAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
+P + L A LRL++ + +A +S A R+ V E L+ G T L+D+
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEV LKAPRPGQLITQLLDT 201

Query: 166 RLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREHLGPIASGAHKLVRFASQG 225
RLV + S W++FDV+ AV W V V + P G H + +
Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAGQDCDP-----EAPMTEGTR----CCRQEMYIDLQGM 275
P GE +L L L +G G P +P G + C R +Y+D +
Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSRQGRKRNRCRRHALYVDFSDV 315

Query: 276 KWAKNWWLEPPGFLAYECVGTCQQP 300
W +W++ PPG+ AY C G C P
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECFPF 339

tr Q8JIJ6 **Bmp4 protein [Bmp4] [Labidochromis caeruleus (blue streak hap)]** 403 AA
align

Score = 66.2 bits (160), Expect = 9e-10
Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLRFQEPVPKAAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
+P + L A LRL++ + +A +S A R+ V E L+ G T L+D+
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEV LKAPRPGQLITQLLDT 201

Query: 166 RLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREHLGPIASGAHKLVRFASQG 225
RLV + S W++FDV+ AV W V V + P G H + +
Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--ARERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAGQDCDP-----EAPMTEGTR----CCRQEMYIDLQGM 275
P GE +L L L +G G P +P G + C R +Y+D +
Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSRQGRKRNRCRRHALYVDFSDV 315

Query: 276 KWAKNWWLEPPGFLAYECVGTCQQP 300
W +W++ PPG+ AY C G C P
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECFPF 339

tr Q8JIJ2 **Bmp4 protein [Bmp4] [Tilapia rendalli (redbreast tilapia)]** 403 AA
align

Score = 66.2 bits (160), Expect = 9e-10
Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLRFQEPVPKAAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
+P + L A LRL++ + +A +S A R+ V E L+ G T L+D+
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEV LKAPRPGQLITQLLDT 201

Query: 166 RLVS VHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREHLGPLASGAHKLVRFASQG 225
RLV + S W++FDV+ AV W V V + P G H + +
Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--THERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP-----EAPMTEGTR----CCRQEMYIDLQGM 275
P GE +L L L +G G P +P G + C R +Y+D +
Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSRQGRKRNRCRRHALYVDFSDV 315

Query: 276 KWAKNWVLEPPGFLAYECVGTCQQP 300
W +W++ PPG+ AY C G C P
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECFPF 339

tr Q8JFE2 **Bmp4 protein [Bmp4] [Boulengerochromis microlepis (Giant cichlid)]** 403
AA
align

Score = 66.2 bits (160), Expect = 9e-10
Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLRFQEPVPKAAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
+P + L A LRL++ + +A +S A R+ V E L+ G T L+D+
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEV LKAPRPGQLITQLLDT 201

Query: 166 RLVS VHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREHLGPLASGAHKLVRFASQG 225
RLV + S W++FDV+ AV W V V + P G H + +
Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP-----EAPMTEGTR----CCRQEMYIDLQGM 275
P GE +L L L +G G P +P G + C R +Y+D +
Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSRQGRKRNRCRRHALYVDFSDV 315

Query: 276 KWAKNWVLEPPGFLAYECVGTCQQP 300
W +W++ PPG+ AY C G C P
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECFPF 339

tr Q8JIJ7 **Bmp4 protein [Bmp4] [Julidochromis transcriptus]** 403 AA
align

Score = 65.9 bits (159), Expect = 1e-09
Identities = 59/205 (28%), Positives = 88/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLRFQEPVPKAAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
+P + L A LRL++ + +A +S A R+ V E L+ G T L+D+
Sbjct: 145 IPVDELLSSAELRLYRHQIDEAIADA---ISDDQALHRINVYEV LKAPRPGQLITQLLDT 201

Query: 166 RLVS VHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREHLGPLASGAHKLVRFASQG 225
RLV + S W++FDV+ AV W V V + P G H + +
Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP-----EAPMTEGTR----CCRQEMYIDLQGM 275
P GE +L L L +G G P +P G + C R +Y+D +
Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSRQGRKRNRCRRHALYVDFSDV 315

Query: 276 KWAKNWWLEPPGFLAYECVGTCQQP 300
W +W++ PPG+ AY C G C P
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECFPF 339

tr Q8JIJ3 **Bmp4 protein [Bmp4] [Tropheus duboisi]** 403 AA
align

Score = 65.5 bits (158), Expect = 1e-09
Identities = 59/205 (28%), Positives = 87/205 (41%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLRFQEPVPKAAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
+P + L A LRL++ + +A +S A R+ V E L+ G T L+D+
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIAADA---ISDDQALHRINVEVLKAPRPGQLITQLLDT 201

Query: 166 RLVS VHESGWKAFDVTEAVNFWXXXXXXXXXXXXXSVQREHLGPLASGAHKLVRFASQG 225
RLV S W++FDV+ AV W V V + P G H + +
Sbjct: 202 RLVRHDASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGRHVRISRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP-----EAPMTEGTR----CCRQEMYIDLQGM 275
P GE +L L L +G G P +P G + C R +Y+D +
Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSRQGRKRNRNCRRHALYVDFSDV 315

Query: 276 KWAKNWWLEPPGFLAYECVGTCQQP 300
W +W++ PPG+ AY C G C P
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECFPF 339

tr Q90YJ3 **Anti-dorsalizing morphogenetic protein [admp] [Brachydanio rerio (Zebrafish) (Danio rerio)]** 391 AA
align

Score = 65.1 bits (157), Expect = 2e-09
Identities = 63/231 (27%), Positives = 92/231 (39%), Gaps = 63/231 (27%)

Query: 110 NSELVQAVLRLRFQ-EPVPKAAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTS----LID 164
+ +++ A L LF+ P L+RH V +V D G S L+
Sbjct: 118 SEKILTAELHLFLKLRPKTSIVLNRHHFCQ-----VSVYQVLDSGKKNVSQGKKLLS 168

Query: 165 SRLSV VHESGWKAFDVTEAVNFWXXXXXXXXXXXXXSVQREHLGPLAS-----GAH--- 216
SRLV +H +GW+ F +T+AV W +S + +LG L S G+
Sbjct: 169 SRLVPIHSTGWVFTITQAVRSW-----MSDEGSNLGLLVSVRTLQSGMDL 215

Query: 217 KLVRFASQGAPAGLGEPQLELHTLD-----LRDYGAQGDCDPEAPMT----- 258
K+VRFAS +P L L T D L D P +P
Sbjct: 216 KMRVFASGRDHHHSKQPMVLVFTDDGRRRAASLEATSKGSDVSPGSPSQPLPSVPASRRSP 275

Query: 259 -----EGTRCCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300
E C RQ +Y+D + + W+ W++ P G+ AY C G+C P
Sbjct: 276 RSVDYDERGEKMACQRQPLYVDFFEEIGWS-GWIVSPKGYNAYHCKGSCIFP 325

tr Q8JIK0 **Bmp4 protein [Bmp4] [Cyprichromis leptosoma]** 403 AA

align

Score = 64.7 bits (156), Expect = 3e-09

Identities = 58/205 (28%), Positives = 87/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLRFQEPVPKAAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
+P + L A LRL++ + +A +S R+ V E L+ G T L+D+

Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIAADA---ISDDQXLHRINVYEV LKAPRPGQLITQLLDT 201

Query: 166 RLVS VHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREHLGLASGAHKLVRFASQG 225
RLV + S W++FDV+ AV W V V + P G H + +

Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTPRHQGQHVRI SRSLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP-----EAPMTEGTR----CCRQEMYIDLQGM 275
P GE +L L L +G G P +P G + C R +Y+D +

Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSRQGRKRNRNCRRHALYVDFSDV 315

Query: 276 KWAKNWWLEPPGFLAYECVGTCCQP 300

W +W++ PPG+ AY C G C P

Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECPPF 339

sp P21275 Bone morphogenetic protein 4 precursor (BMP-4) (BMP-2B) 408
BMP4_MOUSE [Bmp4] [Mus
musculus (Mouse)] AA
align

Score = 64.3 bits (155), Expect = 3e-09

Identities = 59/226 (26%), Positives = 87/226 (38%), Gaps = 32/226 (14%)

Query: 92 SEASTHLLVFGMEQRLPPNSELVQAVLRLRFQEPVPKA-----ALHRHGRLSPRSAQARVT 146
SE+S +F + +P N + A LRLF+E V + HR A +

Sbjct: 134 SESSAFRFLFNLS-IPENEVISSAELRLFREQVDQGPDWEQGFHRINIYEV MKPPAEMV 192

Query: 147 VEWLVRDDGSNRTSLIDSRLVS VHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQRE 206
G T L+D+RLV + + W+ FDV+ AV W + V

Sbjct: 193 -----PGHLITRLLDTRLVHHNVTRWETFDVSPAVLRW--TREKQPNYGLAIEVTHL 242

Query: 207 HLGPLASGAHKLVRFASQGAPAGLGE-----PQLEL-----HTLDRDYGAQGDCDPE 254
H G H + S+ P G G+ P L HTL R P+

Sbjct: 243 HQTRTHQGQHVRI---SRSLPQSGDWAQLRPLLVTFGHDGRGHTLTRRRAKRSPKHPQ 299

Query: 255 APMTEGTRCCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCCQP 300

+ C R +Y+D + W +W++ PPG+ A+ C G C P

Sbjct: 300 RSRKKNKNCRRHS LYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPPF 344

tr Q8JIJ5 Bmp4 protein [Bmp4] [Oreochromis niloticus (Nile tilapia) 403
(Tilapia
nilotica)] AA
align

Score = 64.3 bits (155), Expect = 3e-09

Identities = 58/205 (28%), Positives = 87/205 (42%), Gaps = 21/205 (10%)

Query: 107 LPPNSELVQAVLRLRFQEPVPKAAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
+P + L A LRL++ + +A +S R+ V E L+ G T L+D+

Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIADA---ISHDQGLHRINVYEV LKAPRPGQLITQLLDT 201

Query: 166 RLVS VHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREHLGPLASGAHKLVRFASQG 225
 RLV + S W++FDV+ AV W V V + P G H + +

Sbjct: 202 RLVRHNASRWESFDVSPAVLRW--TRERLPNYGLAVEVLHLNQTTPRHQGRHVIRISRLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDP-----EAPMTEGTR----CCRQEMYIDLQGM 275
 P GE +L L L +G G P +P G + C R +Y+D +

Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKGHPLTRRTKRSRQGRKRNRNCRRHLYVDFSDV 315

Query: 276 KWAKNWVLEPPGFLAYECVGTCCQP 300
 W +W++ PPG+ AY C G C P

Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECFP 339

tr Q8UVQ2 **Anti-dorsalizing morphogenetic protein [admp] [Brachydanio rerio** 391
(Zebrafish) (Danio rerio)] AA
align

Score = 63.5 bits (153), Expect = 6e-09
 Identities = 61/227 (26%), Positives = 91/227 (39%), Gaps = 55/227 (24%)

Query: 110 NSELVQAVLRLFQ-EPVPKAAALHRHGR LSPRSAQARVTVEWLRVRDDGSNRTSLIDSRLV 168
 + +++ A L LF+ P L+RH Q V + + S L+ SRLV

Sbjct: 118 SEKILTAELHLFKLRPKTSIVLNRH-----HFCQVSVYQVLDSSKKNVSQGGKLLSSRLV 172

Query: 169 SVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREHLGPLAS-----GAH---KLVR 220
 +H +GW+ F +T+AV W +S + +LG L S G+ K+VR

Sbjct: 173 PIHSTGWEVFTITQAVRSW-----MSDEGSNLGLLVSVRTLQAGSMDLKMVR 219

Query: 221 FASQGAPAGLGEPQLELHTLDLR-----DYGAQGDCDPEAPMTEGTR----- 262
 FAS +P L L T D R D G P + R

Sbjct: 220 FASGRDHHHSKQPMVLVFTDDGRRRAASLEATSKGSDVSPGGSSQPLPSVPASRRSSRSVD 279

Query: 263 -----CCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCCQP 300
 C RQ +Y+D + + W+ W++ P G+ AY C G+C P

Sbjct: 280 YDERGEKMACRQRP LYVDFEIEIGWS-GWIVSPKGYNAYHCKGSCIFP 325

tr Q91597 **Anti-dorsalizing morphogenetic protein 1 precursor [Xenopus laevis** 390
(African clawed frog)] AA
align

Score = 63.2 bits (152), Expect = 7e-09
 Identities = 56/217 (25%), Positives = 86/217 (38%), Gaps = 38/217 (17%)

Query: 110 NSELVQAVLRLFQ---EPVPKAAALHRHGR LSPRSAQARVTVEWLRVRDDGSNRTSLIDSR 166
 N +++ A L LF+ P +A RH Q V + + + L+ S+

Sbjct: 120 NEKILTAELHLFKLKPRPSEQAYFKRH-----HFCQISVYMLVDKNKIQLPQGRKLLSSK 174

Query: 167 LVS VHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREHLGPLASGAHKLVRFASQGA 226
 LV +H SGW+ F +T+AV W ++ + P ++RFAS

Sbjct: 175 LVPIHSSGWEVFSITQAVRAWNDESANHGILVTVRNLGGAQVDP-----NIIRFASGRD 228

Query: 227 PAGLGEPQLELHTLDLR----DYGAQGDCD-----PEAPMTEGTR-----C 263

```

      + P L L T D R      Q D      P A P + T R      C
Sbjct: 229 HHESKQPMVLVLTDDGRRGIVSVNNQPDDQLMPLPNVPMAPTSNRTRLGRSVEEDGQLPC 288

Query: 264 CRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCCQP 300
      R +Y+D + + W+ W++ P G+ AY C G+C P
Sbjct: 289 QRHPLYVD FEEIGWS-GWII SPRGYNAYHCKGSCFP 324

```

tr Q8UVQ8 **Anti-dorsalizing morphogenetic protein [admp] [Brachydanio rerio (Zebrafish) (Danio rerio)]** 391 AA align

Score = 63.2 bits (152), Expect = 7e-09
Identities = 61/227 (26%), Positives = 91/227 (39%), Gaps = 55/227 (24%)

```

Query: 110 NSELVQAVLRLFQ-EPVPKAAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSLIDSRLV 168
      + +++ A L LF+ P L+RH Q V + + S L+ SRLV
Sbjct: 118 SEKILTAELHLFLKLRPKTSIVLNRH-----HFCQVSVYQVLDSSKKNVSQGGKLLSSRLV 172

Query: 169 SVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXSVQREHLGPLAS-----GAH---KLVR 220
      +H +GW+ F +T+AV W +S + +LG L S G+ K+VR
Sbjct: 173 PIHSTGWEVFTITQAVRSW-----MSDEGSNLGLLVSVRTLQAGSMDLKMVR 219

Query: 221 FASQGAPAGLGEPQLELHTLDLR-----DYGAQGDCDPEAPMTEGTR----- 262
      FAS +P L L T D R D G P + R
Sbjct: 220 FASGRDHHHSKQPMVLVLTDDGRRRAASLEATSKGSDVSPGGXSQPLPSVPASRRSSRSVD 279

Query: 263 -----CCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCCQP 300
      C RQ +Y+D + + W+ W++ P G+ AY C G+C P
Sbjct: 280 YDERGEKMACQRQPLYVD FEEIGWS-GWIVSPKGYNAYHCKGSCIFP 325

```

tr Q8JIJ8 **Bmp4 protein [Bmp4] [Haplochromis nyererei]** 403 AA align

Score = 63.2 bits (152), Expect = 7e-09
Identities = 58/205 (28%), Positives = 87/205 (42%), Gaps = 21/205 (10%)

```

Query: 107 LPPNSELVQAVLRLFQEPVPKAAALHRHGRLSPRSAQARVTV-EWLRVRDDGSNRTSLIDS 165
      +P + L A LRL++ + +A +S A R+ V E L+ G T L+D+
Sbjct: 145 IPEDELLSSAELRLYRHQIDEAIAA---ISDDQALHRINVEVLKAPRPGQLITQLLDT 201

Query: 166 RLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXSVQREHLGPLASGAHKLVRFASQG 225
      RLV + S W++FDV+ AV W V V + P G H + +
Sbjct: 202 RLVHRNASRWESFDVSPAVLRW--ARERLPNYGLAVEVLHLNQTTPRHQGRHVIRISRLHQ 259

Query: 226 APAGLGEPQLELHTLDLRDYGAQGD-----CDPEAPMTEGTR----CCRQEMYIDLQGM 275
      P GE +L L L +G G +P G + C R +Y+D +
Sbjct: 260 EP---GEDWEQLRPL-LVTFGHDGKHSLTRRTKRSRQRGRKRNRCRRHALYVDFSDV 315

Query: 276 KWAKNWWLEPPGFLAYECVGTCCQP 300
      W +W++ PPG+ AY C G C P
Sbjct: 316 GW-NDWIVAPPGYQAYYCHGECFP 339

```

tr Q811S3 Bone morphogenetic protein 4 [Bmp4] [Rattus norvegicus (Rat)] 408 AA

align

Score = 62.8 bits (151), Expect = 1e-08

Identities = 59/226 (26%), Positives = 85/226 (37%), Gaps = 32/226 (14%)

Query: 92 SEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKA-----ALHRHGRLSPRSAQARVT 146
SE+S F + +P N + A LRLF+E V + HR A +
Sbjct: 134 SSSAFRFFFNLS-IPENEVISSAELRLFREQVDQGPDWEQGFHRINIYEVMPKPAEMV 192

Query: 147 VEWLVRVDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXSVVQRE 206
G T L+D+RLV + + W+ FDV+ AV W + V
Sbjct: 193 -----PGHLITRLLDTRLVRHNVTRWETFDVSPAVLRW--TREKQPNYGLAIEVTHL 242

Query: 207 HLGPLASGAHKLVRFASQGAPAGLG-----EPQLEL-----HTLDRDYGAQGDCDPE 254
H G H + S+ P G G P L HTL R P+
Sbjct: 243 HQTRTHQGQHVRI---SRSLPQSGNWAQLRPLLVTFGHDGRGHTLTRRRAKRSPKHHPQ 299

Query: 255 APMTEGTRCCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300
+ C R +Y+D + W +W++ PPG+ A+ C G C P
Sbjct: 300 RSRKKNKNCRRHSLYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 344

tr Q6AYU9 Bmp4 protein [Bmp4] [Rattus norvegicus (Rat)] 408 AA

align

Score = 62.8 bits (151), Expect = 1e-08

Identities = 59/226 (26%), Positives = 85/226 (37%), Gaps = 32/226 (14%)

Query: 92 SEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKA-----ALHRHGRLSPRSAQARVT 146
SE+S F + +P N + A LRLF+E V + HR A +
Sbjct: 134 SSSAFRFFFNLS-IPENEVISSAELRLFREQVDQGPDWEQGFHRINIYEVMPKPAEMV 192

Query: 147 VEWLVRVDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXSVVQRE 206
G T L+D+RLV + + W+ FDV+ AV W + V
Sbjct: 193 -----PGHLITRLLDTRLVHHNVTRWETFDVSPAVLRW--TREKQPNYGLAIEVTHL 242

Query: 207 HLGPLASGAHKLVRFASQGAPAGLG-----EPQLEL-----HTLDRDYGAQGDCDPE 254
H G H + S+ P G G P L HTL R P+
Sbjct: 243 HQTRTHQGQHVRI---SRSLPQSGNWAQLRPLLVTFGHDGRGHTLTRRRAKRSPKHHPQ 299

Query: 255 APMTEGTRCCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300
+ C R +Y+D + W +W++ PPG+ A+ C G C P
Sbjct: 300 RSRKKNKNCRRHSLYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 344

tr Q8AYB5 Bone morphogenetic protein 4 (Fragment) [Oryzias latipes
(Medaka
fish) (Japanese ricefish)]

392

AA

align

Score = 62.0 bits (149), Expect = 2e-08

Identities = 58/216 (26%), Positives = 92/216 (41%), Gaps = 19/216 (8%)

Query: 95 STHLLVFGMEQRLPPNSELVQAVLRLRFQEPVPKAAALHRHGRLSPRSAQARVTVEWLRVRD 154
S HL +P + L A LRL+++ + +A + L+ + E L+
Sbjct: 133 SIHLRFLFNLSSIPEDELLSSAELRLYRQQLGEA--NDDSPNDQGLHRINIYEVLKPPR 190

Query: 155 DGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXSVQREHLGPLASG 214
G T L+D+RLV + S W++FDV+ AV W ++V+ HL
Sbjct: 191 PGQLITQLLDTRLVHHNASRWESFDVSPAVLRW----TRERLPNYGLAVEILHLNQTPHN 246

Query: 215 AHKLVRFASQGAPAGLGEPQLELHTLDLRDYGAQGD-----CDPEAPMTEGTR----CC 264
H+ VR S+ GE ++ L L +G G +P G + C
Sbjct: 247 QHRHVRI-SRSLHQEPGEDWDQVRPL-LVTFGHDGKGHSLTRRTKRSPKPRGRKRNCR 304

Query: 265 RQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300
R +Y+D + W +W++ PPG+ AY C G C P
Sbjct: 305 RHTLYVDFSDVGW-NDWIVAPPGYQAYYCHGECFPF 339

tr P87380 **Bone morphogenetic protein-4 (Fragment) [bmp4] [Brachydanio** 391
rerio AA
(Zebrafish) (Danio rerio)] align

Score = 61.6 bits (148), Expect = 2e-08
Identities = 48/163 (29%), Positives = 70/163 (42%), Gaps = 17/163 (10%)

Query: 148 EWLVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXSVQREH 207
E L+ +G T L+D+RLV + S W++FDV+ AV W V V +
Sbjct: 180 EVLKAPREGQLITQLLDTRLVRHNTSKWESFDVSPAVLRW--TQEKRSNHGLAVEVVQMK 237

Query: 208 LGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLRDYGAQGDCDP-----EAPMTEGT 261
P+ G H V + P E +L L L +G G P +P G
Sbjct: 238 RNPVQKGRHVRVRSRVHPLP---DEEWDQLRPL-LVTFGHDGKSHPLTRRAKRSPKQGR 293

Query: 262 R----CCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300
+ C R +Y+D + W +W++ PPG+ AY C G C P
Sbjct: 294 KRNRCRRHALYVDFSDVGW-NDWIVAPPGYQAYYCHGECFPF 335

tr O57574 **Bone genetic protein 4 (Hypothetical protein) (Bone** 400
morphogenetic AA
protein 4) [bmp4] [Brachydanio rerio (Zebrafish) (Danio align
rerio)]

Score = 61.6 bits (148), Expect = 2e-08
Identities = 48/163 (29%), Positives = 70/163 (42%), Gaps = 17/163 (10%)

Query: 148 EWLVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXSVQREH 207
E L+ +G T L+D+RLV + S W++FDV+ AV W V V +
Sbjct: 181 EVLKAPREGQLITQLLDTRLVRHNTSKWESFDVSPAVLRW--TQEKRSNHGLAVEVVQMK 238

Query: 208 LGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLRDYGAQGDCDP-----EAPMTEGT 261
P+ G H V + P E +L L L +G G P +P G
Sbjct: 239 RNPVQKGRHVRVRSRVHPLP---DEEWDQLRPL-LVTFGHDGKSHPLTRRAKRSPKQGR 294

Query: 262 R----CCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300
+ C R +Y+D + W +W++ PPG+ AY C G C P

Sbjct: 295 KRNRNCRRHALYVDFSDVGW-NDWIVAPPGYQAYYCHGECFPF 336

tr Q6J3S5 **Bone morphogenetic protein 24B [BMP24B] [Petromyzon marinus** 451
(Sea AA
lamprey)] align

Score = 61.2 bits (147), Expect = 3e-08

Identities = 67/287 (23%), Positives = 109/287 (37%), Gaps = 33/287 (11%)

Query: 45 RADMEKLV---IPAHVRAQYVLLRRSHGDRS--RGKRFSQS FREVAGRFLASEASTHLL 99
RAD E++ + + V R + G + RG +S +++ + +T

Sbjct: 103 RADKERVGKDDVDVEEEKEEVAFPREAQGRANTVRGFHHDESTKLSLGQSTEDGTTWHF 162

Query: 100 VFGMEQRLPPNSELVQAVLRLFQEPV--PKAALHRHGRLSPRSAQARVTVEWLRVRDDGS 157
+F + +P + E+ A LR+ V P + L+PR + V

Sbjct: 163 LFNLS--IPDSEEVTAELRVHHTRVHSPCPSSSPACELAPRLERINVYEVVAPPSSPSG 221

Query: 158 NRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXV-SVQREHLGPLASGAH 216
+ L+D+R+V +ES W+AFDV+ AV+ W V V+R G A+G

Sbjct: 222 AASRLLDTRVVRTNESRWEAFDVSPAVSRWTRGSAPNRGFAVEVLPVRRPSGGVAANGVP 281

Query: 217 KLVRFASQGAPAGLGEPQLELHTLDLRDYGAQGDCDPEAPMTEGTR----- 262
A + P H + R D AP T +R

Sbjct: 282 SEAVLAQPRSGVASLFPDGDGSHQTEPRLLVTFGSDGRAPFTPRSRARRSIGGAPRQAAH 341

Query: 263 -----CCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300

C R +Y+D + + W +W++ PPG+ AY C G C P

Sbjct: 342 KARRKPRYSRRHALYVDFREVGW-NDWIVAPPGYHAYFCHGECFPF 387

tr O13107 **BMP4 [bmp4] [Brachydanio rerio (Zebrafish) (Danio rerio)]** 400 AA
align

Score = 60.8 bits (146), Expect = 4e-08

Identities = 47/163 (28%), Positives = 69/163 (41%), Gaps = 17/163 (10%)

Query: 148 EWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXSVQREH 207
E L+ +G T L+D+RLV + S W++FDV+ AV W V V +

Sbjct: 181 EVLKAPREGQLITQLLDTRLVRPNTSKWESFDVSPAVLRW--TQEKRSNHGLAVEVVQMK 238

Query: 208 LGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLRDYGAQGDCDP-----EAPMTEGT 261
P+ G H V + P E + L L +G G P +P G

Sbjct: 239 RNPVQKGRHARVSRSVHPLP---NEEWDHVRPL-LVTFGHDGKSHPLTRRAKRSPKQRGR 294

Query: 262 R----CCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300

+ C R +Y+D + W +W++ PPG+ AY C G C P

Sbjct: 295 KRNRNCRRHALYVDFSDVGW-NDWIVAPPGYQAYYCHGECFPF 336

tr Q9XYQ8 **Bone morphogenetic protein BMP2/4 (Fragment) [BMP2/4]** 289 AA
[Strongylocentrotus purpuratus (Purple sea urchin)] align

Score = 60.8 bits (146), Expect = 4e-08
Identities = 57/222 (25%), Positives = 88/222 (38%), Gaps = 34/222 (15%)

Query: 107 LPPNSELVQAVLRLRFQEP-----VPKALHRHGRSLSPRSAQARVTVEWLRVRDDGSNRT 160
+P + A LRLF++ V + ALH L P R+ V + ++ NR
Sbjct: 7 MPEEEVMTTAE LRLFRKDLDEHHIVKRHALHDRES LKPIHYMQRINVYHI-LKPVARNRD 65

Query: 161 S---LIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREHLGPLASGAHK 217
+ LID+RLV V + W++FDV A+ W + R P H
Sbjct: 66 TIKRLIDTRLVDVRNASWESFDVRPAMRVWLEEPEKNHGLEIELIDSRGRPSP----NH 121

Query: 218 LVRFASQGAPAGLGE-----PQLELHTLDRDYGAQGDCDP--EAPMTEGTR 262
VR + P+ + E PQ+ ++ D R + +G R
Sbjct: 122 HVRVTREADPSKVEELENEEDRWVFQTRPQIVTYSDDGRTKRSPSSSSSGRGQKKRKGKR 181

Query: 263 ----CCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300
C R E+Y+D + W +W++ P G+ AY C G C P
Sbjct: 182 LKANCRRHELYVDFSDVHW-NDWIVAPAGYQAYYCRGECPPF 222

sp Q90752 **Bone morphogenetic protein 4 precursor (BMP-4) [BMP4]** 405
BMP4_CHICK **[Gallus** AA
gallus (Chicken)] align

Score = 60.5 bits (145), Expect = 5e-08
Identities = 62/224 (27%), Positives = 93/224 (40%), Gaps = 31/224 (13%)

Query: 92 SEASTHLLVFGMEQRLPPNSELVQAVLRLRFQEPV--PKAALHRHGRSLSPRSAQARVTV-E 148
SEA VF + +P N + LRL++E V P AA R R+ + E
Sbjct: 134 SEAPRIRFVFNLS-VPDNEVISSEELRLRYREQVEEPSAAWERGFI-----RINIYE 184

Query: 149 WLRVRDDGSNR-TSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREH 207
++ + S T L+D+RLV + + W+ FDV+ AV W + V H
Sbjct: 185 VMKPLSERSQAITRLLDTRLVHHNVTRWETFVSPAVIRW--TKDKQPNHGLVIEVTHLH 242

Query: 208 LGPLASGAHKLVRFASQGAPAGLGE PQLELHTLDRDYGAQGDCDP-----EAPMTEGT 261
G H + S+ P G G +L L L +G G +P G+
Sbjct: 243 QAQTHQGKHVRI---SRSLPQGHGGDWAQLRPL-LVTFGHDGRGHALTRRARRSPKHHGS 298

Query: 262 R-----CCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300
R C R +Y+D + W +W++ PPG+ A+ C G C P
Sbjct: 299 RKNKKNCRRHLYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPPF 341

sp P25703 **Bone morphogenetic protein 2-I precursor (BMP-2-I)** 398
BMPA_XENLA **[Xenopus laevis** AA
(African clawed frog)] align

Score = 59.3 bits (142), Expect = 1e-07
Identities = 59/210 (28%), Positives = 89/210 (42%), Gaps = 35/210 (16%)

Query: 109 PNSELV-QAVLRLRFQEPVVK-----AALHR---HGRSLSPRSAQARVTVEWLRVRDDGSN 158
PN ELV A LR+F+E V + + LHR + + P +A +R V
Sbjct: 142 PNEELVTS AELRIFREQVQEPFESDSSKLHRINIYDIVKAAAASRGPV----- 190

Query: 159 RTSLIDSRLVSVHESGWKAFDVT EAVNFWXXXXXXXXXXXXXSVQREHLGPLASGAHKL 218
L+D+RLV +ES W++FDVT A+ W V+ HL + K
Sbjct: 191 -VRLLDTRLVHHNESKWESFDVTPAIARWIAHKQPNHGFV----VEVNHLNDNDKNVPKKH 245

Query: 219 VRFASQGAPAGLGE PQ----LELHTLDLRDYGAGQDCDPEAPMTEGTR----CCRQEMYI 270
VR + P PQ L + D + + +A + R C R +Y+
Sbjct: 246 VRISRSLTPDKDNWPQIRPLLVTFSHDGKGHALHKRQKRQARHKQKRKLKSSCRRHPLYV 305

Query: 271 DLQGMKWAKNWNVLEPPGFLAYECVGT CQP 300
D + W +W++ PPG+ A+ C G C P
Sbjct: 306 DFSDVGW-NDWIVAPPGYHAFYCHGECPPF 334

tr Q8MJV5 **Bone morphogenetic protein 4 [sBmp4] [Suncus murinus (House** 409
shrew) AA
(Musk shrew)] align

Score = 58.5 bits (140), Expect = 2e-07
Identities = 58/227 (25%), Positives = 84/227 (36%), Gaps = 33/227 (14%)

Query: 92 SEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPV PKA-----ALHRHGRLSPRSAQARVT 146
SE S F + +P N + A LRLF+E V + HR A V
Sbjct: 134 SENS AFRFFFNLS-IPENEVISSAELRLFREQVDQGP DWEQGFHRINIYEV MKPPAEVV 192

Query: 147 VEWLVRVDDGNSRTSLIDSRLVSVHESGWKAFDVT EAVNFWXXXXXXXXXXXXXSVQRE 206
G T L+D+RLV + + W+ FDV+ AV W + V
Sbjct: 193 -----PGHLITRLLDTRLVHHNVTRWETF DVS PAVLRW--TREKQPNYGLAIEVTHL 242

Query: 207 HLGPLASGAHKLVRFASQGAPAGLGE-----PQLELHTLDLRDYG-----AQGDCDP 253
H G H + S+ P G G+ P L D R + P
Sbjct: 243 HQTRTHQGQHVRI---SRSLPQNGDWAQLRPLLVTFGHDGRGHALTRRRRAKRSPKHHP 299

Query: 254 EAPMTEGTRCCCRQEMYIDLQGMKWAKNWNVLEPPGFLAYECVGT CQP 300
+ + C R +Y+D + W +W++ PPG+ A+ C G C P
Sbjct: 300 QRARKKNKNCRRHSLYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPPF 345

sp P49001 **Bone morphogenetic protein 2 precursor (BMP-2) (BMP-2A)** 393
BMP2_RAT [Bmp2] AA
[Rattus norvegicus (Rat)] align

Score = 57.4 bits (137), Expect = 4e-07
Identities = 54/211 (25%), Positives = 89/211 (41%), Gaps = 35/211 (16%)

Query: 107 LPPNSELVQAVLRLFQEPV PKAALHRHGRLSPRSAQARVTVEWLVRVDDGNSR---TSLI 163
+P + L A L++F+E + +A L S Q R+ + + S++ T L+
Sbjct: 137 VPTDEFLTSAELQIFREQMQEA-----LGNSSFQHRINIYEIIKPATASSKFPVTRLL 189

Query: 164 DSRLVSVHESGWKAFDVT EAVNFWXXXXXXXXXXXXXSVS-----VQREHLGPLASGAH 216
D+RLV+ + S W++FDVT AV W V+ V + H+ ++ H
Sbjct: 190 DTRLVTQNTSQWESFDVTPAVMRWTAQGHTNHGFVVEVAHLEEKPGVSKRHV-RISRSLH 248

Query: 217 KLVRFASQGAPA-----GLGEPQLELHTLDLRDYGAGQDCDPEAPMTEGTRCCCRQEMY 269
+ SQ P G G P LH + R + + C R +Y
Sbjct: 249 QDEHSWSQVRPLLVTFGHDGKGHP---LHKREKR-----QAKHKQKRKLKSSCKRHPLY 299

Query: 270 IDLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300
+D + W +W++ PPG+ A+ C G C P
Sbjct: 300 VDFSDVGW-NDWIVAPPGYHAFYCHGECFPF 329

sp P21274 **Bone morphogenetic protein 2 precursor (BMP-2) (BMP-2A)** 394
BMP2_MOUSE [Bmp2] [Mus AA
musculus (Mouse)] align

Score = 57.4 bits (137), Expect = 4e-07
Identities = 54/211 (25%), Positives = 89/211 (41%), Gaps = 35/211 (16%)

Query: 107 LPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNR----TSL 162
+P + L A L++F+E + +A L S Q R+ + + ++ +N T L
Sbjct: 138 VPSDEFLTSAELQIFREQIQEA-----LGNSSFQHRINIYEI-IKPAAANLKFPVTRL 189

Query: 163 IDSRLVSVHESGWKAFDVTAVNFWXXXXXXXXXXXXXSVQREHLG-----PLASGAH 216
+D+RLV+ + S W++FDVT AV W V+ E+ G ++ H
Sbjct: 190 LDTRLVNQNTSQWESFDVTPAVMRWTTQGHNTNHGFVVEVAHLEENPGVSKRHVRISRSLH 249

Query: 217 KLVRFASQGAPA-----GLGEPQLELHTLTLRDLRQYGAQGDCEAPMTEGTRCCRQEMY 269
+ S Q P G G P L H + R + + C R +Y
Sbjct: 250 QDEHSWSQIRPLLVTFGHDGKGHP---LHKREKR-----QAKHKQRKRLKSSCKRHPLY 300

Query: 270 IDLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300
+D + W +W++ PPG+ A+ C G C P
Sbjct: 301 VDFSDVGW-NDWIVAPPGYHAFYCHGECFPF 330

tr Q90YD7 **Bone morphogenetic protein 2 (BMP-2) [BMP-2] [Xenopus** 398
tropicalis AA
(Western clawed frog) (Silurana tropicalis)] align

Score = 57.4 bits (137), Expect = 4e-07
Identities = 57/210 (27%), Positives = 88/210 (41%), Gaps = 35/210 (16%)

Query: 109 PNSELV-QAVLRLFQEPVVK-----AALHR---HGRLSPRSAQARVTVEWLRVRDDGSN 158
PN ELV A LR+F+E V + + LHR + + P +A +R V
Sbjct: 142 PNEELVTSaelRIFREGVQEPFEGDSSKLHRINIYDIVKPAASRGPV----- 190

Query: 159 RTSLIDSRLVSVHESGWKAFDVTAVNFWXXXXXXXXXXXXXSVQREHLGPLASGAHKL 218
L+D+RL+ +ES W++FDVT A+ W V+ HL + K
Sbjct: 191 -VRLLDTRLIIHNESKWESFDVTPAIRWIAHKQPNHGFVVEVT----HLDNDKNVPKHH 245

Query: 219 VRFASQGAPAGLG----EPQLELHTLTLRDLRQYGAQGDCEAPMTEGTR----CCRQEMYI 270
VR + P P L + D + + +A + R C R +Y+
Sbjct: 246 VRISRSLVPDKDSWPRIPLLVTFSDHGKGHALHKREKRQARHKQRKRLKSSCRRHPLYV 305

Query: 271 DLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300
D + W +W++ PPG+ A+ C G C P
Sbjct: 306 DFSDVGW-NDWIVAPPGYHAFYCHGECFPF 334

tr Q90YD6 **Bone morphogenetic protein 4 [BMP-4] [Xenopus tropicalis** 400
(Western AA
clawed frog) (Silurana tropicalis)] align

Score = 57.4 bits (137), Expect = 4e-07

Identities = 49/220 (22%), Positives = 90/220 (40%), Gaps = 24/220 (10%)

Query: 92 SEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKALHRHG--RLSPRSAQARVTVEW 149
+E VF + +P N + A LRL++E + G R++ +T
Sbjct: 130 AENGNFRRFVFNLS-IPENEVISSAELRLRYREQIDHGPAWEEGFHRINIYEVMPITAS- 187

Query: 150 LRVRRDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREHLG 209
G + L+D+RL+ + + W++FDV+ A+ W ++++ HL
Sbjct: 188 -----GHMISRLLDTRLIHHNVTQWESFDVSPAIRWTRDKQINHG----LAIEVVHLN 237

Query: 210 PLASGAHKLVRFASQGAPAGLGE-----PQLELHTLDLRDYG----AQGDCEPEAPMTEG 260
+ K VR + P + P L + D R + ++ + P +
Sbjct: 238 QTKTYQGKHVRISRSLLPQEDADWSQMRPLLITFSHDGRGHALTRRSKRSPKQQRPRKKN 297

Query: 261 TRCCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300
C R +Y+D + W +W++ PPG+ A+ C G C P
Sbjct: 298 KHCRRHSlyVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 336

tr Q6PAF3 **LOC397874 protein [LOC397874] [Xenopus laevis (African clawed** 400 AA
frog)] align

Score = 56.6 bits (135), Expect = 7e-07

Identities = 50/220 (22%), Positives = 91/220 (40%), Gaps = 24/220 (10%)

Query: 92 SEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKALHRHG--RLSPRSAQARVTVEW 149
+E VF + +P N + A LRL++E + G R++ +
Sbjct: 130 AENGNFRRFVFNLS-IPENEVISSAELRLRYREQIDHGPAWDEGFHRINIYEVMPKPIAANG 188

Query: 150 LRVRRDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREHLG 209
L + NR L+D+RL+ + + W++FDV+ A+ W ++++ HL
Sbjct: 189 LMI-----NR--LLDTRLIHHNVTQWESFDVSPAIMRWTRDKQINHG----LAIEVIHLN 237

Query: 210 PLASGAHKLVRFASQGAPAGLGE-----PQLELHTLDLRDYG----AQGDCEPEAPMTEG 260
+ K VR + P + P L + D R + ++ + P +
Sbjct: 238 QTKTHQGKHVRISRSLLPQEDADWSQMRPLLITFSHDGRGHALTRRSKRSPKQQRPRKKN 297

Query: 261 TRCCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300
C R +Y+D + W +W++ PPG+ A+ C G C P
Sbjct: 298 KHCRRHSlyVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 336

tr Q91703 **Bone morphogenetic protein 4 [BMP-4] [Xenopus laevis (African** 400 AA
clawed frog)] align

Score = 56.6 bits (135), Expect = 7e-07

Identities = 50/220 (22%), Positives = 91/220 (40%), Gaps = 24/220 (10%)

Query: 92 SEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPAALHRHG--RLSPRSAQARVTVEW 149
 +E VF + +P N + A LRL++E + G R++ +
 Sbjct: 130 AENGNFRLFVNLS-IPENEVISSAELRLRYREQIDHGPWDEGFHRINIYEVMPKPIAANG 188

Query: 150 LRVRRDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREHLG 209
 L + NR L+D+RL+ + + W++FDV+ A+ W +++++ HL
 Sbjct: 189 LMI-----NR--LLDTRLIHNNVTQWESFDVSPAIMRWTRDKQINHG----LAIEVIHLN 237

Query: 210 PLASGAHKLVRFASQGAPAGLGE-----PQLELHTLDLRDYG-----AQGDCEPEAPMTEG 260
 + K VR + P + P L + D R + ++ + P +
 Sbjct: 238 QTKTHQGKHVRISRSLLPQEDADWSQMRPLLITFSHDGRGHALTRRSKRSPKQQRPRKKN 297

Query: 261 TRCCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCCQP 300
 C R +Y+D + W +W++ PPG+ A+ C G C P
 Sbjct: 298 KHCRRHSLYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 336

tr Q9MZV5 **Bone morphogenetic protein 4 (Fragment) [bmp4] [Canis familiaris (Dog)]** 337
 AA
align

Score = 56.6 bits (135), Expect = 7e-07
 Identities = 58/227 (25%), Positives = 85/227 (36%), Gaps = 33/227 (14%)

Query: 92 SEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPK-----AALHRHGRLSPRSAQARVT 146
 SE S +F + +P N + A LRLF+E V + HR A V
 Sbjct: 62 SENSAPFRFLFNLS-IPENEVISSAELRLRFREQVNQDPDWEQGFHRINIYEVMPKPAEVV 120

Query: 147 VEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQRE 206
 G T L+D+RLV + + W+ FDV+ AV W + V
 Sbjct: 121 -----PGHLITRLLDTRLVHHNVTRWETFDVSPAVLRW--TREKQPNYGLAIEVTHL 170

Query: 207 HLGPLASGAHKLVRFASQGAPAGLGE-----PQLEL-----HTLDLRDYGAQG-DCDP 253
 H G H + S+ P G G+ P L H L R +
 Sbjct: 171 HQTRTHQGQHVRI---SRSLPQSGDWAQLRPLLVTFGHDGRGHALTRRQRAKRSPKHHA 227

Query: 254 EAPMTEGTRCCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCCQP 300
 + + C R +Y+D + W +W++ PPG+ A+ C G C P
 Sbjct: 228 QRARKKNKNCRRHSLYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 273

sp P12644 **Bone morphogenetic protein 4 precursor (BMP-4) (BMP-2B)** 408
 BMP4_HUMAN [BMP4] AA
 [Homo sapiens (Human)] align

Score = 56.2 bits (134), Expect = 9e-07
 Identities = 58/227 (25%), Positives = 85/227 (36%), Gaps = 33/227 (14%)

Query: 92 SEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPA-----ALHRHGRLSPRSAQARVT 146
 SE S +F + +P N + A LRLF+E V + HR A V
 Sbjct: 133 SENSAPFRFLFNLS-IPENEVISSAELRLRFREQVDQGPDWERGFHRINIYEVMPKPAEVV 191

Query: 147 VEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQRE 206
 G T L+D+RLV + + W+ FDV+ AV W + V
 Sbjct: 192 -----PGHLITRLLDTRLVHHNVTRWETFDVSPAVLRW--TREKQPNYGLAIEVTHL 241

Query: 207 HLGPLASGAHKLVRFASQGAPAGLG-----EPQLELHTLDLRDYG-----AQGDCDP----- 253
H G H + S+ P G G P L D R + + P
Sbjct: 242 HQTRTHQGQHVRI---SRSLPQSGNWAQLRPLLVTFGHDGRGHALTRRRRAKRSPKHHS 298

Query: 254 EAPMTEGTRCCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
+ + C R +Y+D + W +W++ PPG+ A+ C G C P
Sbjct: 299 QRARKKNKNCRRHSLYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 344

tr Q6J3S6 **Bone morphogenetic protein 24A [BMP24A] [Petromyzon marinus** 422
(Sea AA
lamprey)] align

Score = 56.2 bits (134), Expect = 9e-07
Identities = 81/291 (27%), Positives = 114/291 (38%), Gaps = 50/291 (17%)

Query: 54 PAHVRAQYVVLRRS-HGDRSRGKRFSQSFREVAGRFLASEASTHLLVFGME--QRLPPN 110
P V Y++ L R+ HG S + + + R AS+A+T E + +P +
Sbjct: 74 PGAVVPPYMLQLYRALHGAHSGARDVGRPLDRLVAR-PASQANTVRSFHHDESAEHVPAD 132

Query: 111 SELVQAVLRLRFQ-----EPVPKAALH--RHGRSLSPRSAQA-RVTV-EWLR-VRDDGSN 158
S A LF E + A LH R SP SA R+ V E LR DG+
Sbjct: 133 SGDSTARLLFNVSSIPDGEVITSAELHVYRERLSSPASAGLHRINVYEVLRPAAADGTP 192

Query: 159 RTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXSVSVQREHLGPLASGAHKL 218
L+D+R+V S W+ FDV+ A W + V+ +HL +
Sbjct: 193 IARLLDTRVVHSGRSEWERFDVSPA AVRWAATKEPNHG----LLVEVQHLDGGTPEKRRH 248

Query: 219 VRF-----ASQGAPAGLGEPQLEL-----HTLDLRDYGAGQDCDPEA- 255
VR AS+G G G PQL H RD G P+
Sbjct: 249 VRIGRSLHAEAVAAAARDGASEGGDGGEGWPQLRPLLVTFGHDGKTRDEGTLLRPRPKRN 308

Query: 256 --PMTEGTR----CCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
P G R C R +Y+D + W +W++ PPG+ A+ C G C P
Sbjct: 309 SRPNKGRRGRGQCARYPLYVDFSDVGW-NDWIVAPPGYNAFFCQGECHFP 358

tr Q73818 **Bone morphogenetic protein 4 [BMP-4] [Xenopus laevis (African** 400 AA
clawed frog)] align

Score = 56.2 bits (134), Expect = 9e-07
Identities = 47/205 (22%), Positives = 86/205 (41%), Gaps = 23/205 (11%)

Query: 107 LPPNSELVQAVLRLRFQEPVPKAALHRHG--RLSPRSAQARVTVEWLRVRDDGSNRTSLID 164
+P N + A LRL++E + G R++ + L + NR L+D
Sbjct: 144 IPENEVISSAELRLYREQIDHGPAWDEGFHRINIYEVMPKPIAANGLMI-----NR--LLD 196

Query: 165 SRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXSVSVQREHLGPLASGAHKLVRFASQ 224
+RL+ + + W++FDV+ A+ W +++++ HL + K VR +
Sbjct: 197 TRLIHHNVTQWESFDVSPAIMRWTRDKQINH----LAIEVIHLNQTQKTHQGHVIRISRS 252

Query: 225 GAPAGLG-----PQLELHTLDLRDYG-----AQGDCDPEAPMTEGTRCCCRQEMYIDLQGM 275
P + P L + D R + ++ + P + C R +Y+D +

Sbjct: 253 LLPQEDADWSQMRPLLITFSDHGRGHALTRRSKRSPKQQRPRKKNKHCRRHSLYVDFSDV 312

Query: 276 KWAKNWWLEPPGFLAYECVGTCQQP 300
W +W++ PPG+ A+ C G C P

Sbjct: 313 GW-NDWIVAPPGYQAFYCHGDCPFP 336

tr Q9U418 **Bone morphogenetic protein 2/4 [BMP2/4] [Branchiostoma
belcheri
(Amphoxius)]** 411
AA
align

Score = 55.8 bits (133), Expect = 1e-06
Identities = 54/206 (26%), Positives = 83/206 (40%), Gaps = 18/206 (8%)

Query: 109 PNSELVQAV-LRLFQEPVPKALHRHGRLSPRSAQARVTVEWLRV--RDDGSNRTSLIDS 165
P+ EL++A LRLF+E + + ++G + E +R R + T L+D+

Sbjct: 145 PSVELIKAAELRLFREQIDVDHV-QYGDSTDHHLRVNVYEVMPNSRTNTDTITRLDLD 203

Query: 166 RLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREHLGPLASGAHKLVRFASQG 225
+LV V S W++FDV AV W V V G L++ +L R

Sbjct: 204 KLVDVRNSSWESFDVRSVTKWKNSPERNYGLE--VEVVS PKRGALSNHHVRLRRSTMD 261

Query: 226 APAGLGE-PQLELHTLDLRDYGAQGDCDPEAPMTEGTR-----CCRQEMYIDLQG 274
A P L +T D + G + C R +Y+D

Sbjct: 262 DHAWQHRRPLLLTYTDDGKGSSNSNRVASRQKRANGRKKHQRRRLKANCRRHSLYVDFSD 321

Query: 275 MKWAKNWWLEPPGFLAYECVGTCQQP 300
+ W +W++ PPG+ AY C G C P

Sbjct: 322 VGW-NDWIVAPPGYQAYYCHGECFP 346

sp O46576 **Bone morphogenetic protein 4 precursor (BMP-4) [BMP4]** 409
BMP4_RABIT **[Oryctolagus
cuniculus (Rabbit)]** AA
align

Score = 55.5 bits (132), Expect = 2e-06
Identities = 58/224 (25%), Positives = 84/224 (36%), Gaps = 27/224 (12%)

Query: 92 SEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKA-----ALHRHGRLSPRSAQARVT 146
SE S +F + +P N + A LRLF+E V + HR A

Sbjct: 134 SENSAPFRFLNLSS-IPENEAISAE LRLFREQVDQGPDWERGFHRINIYEVMPKPAEAV 192

Query: 147 VEWLRVRDDGSNRTSLIDSR LSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQRE 206
G T L+D+RLV + + W+ FDV+ AV W V V

Sbjct: 193 -----PGHLITRLLDTRLVHHNVTRWETFDVSPAVLRW--TREKQPNHGLAVEVTHF 242

Query: 207 HLGPLASGAH-KLVRFASQGAPAGLGE PQLEL-----HTLDLRDYGAQG-DCDPEAP 256
H G H +L R QG+ L + H L R + P+

Sbjct: 243 HHTRTHQGQHVRLSRSL LQGSGDWAQFRPLLVTFGHDGRGHALTRRRRAKRS LKHHHPQRA 302

Query: 257 MTEGTRCCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300
+ C R +Y+D + W +W++ PPG+ A+ C G C P

Sbjct: 303 RKKNKNCRRHALYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 345

tr Q90Y82 **LjBmp2/4a (Fragment) [LjBmp2/4a] [Lampetra japonica (Japanese lamprey) (Entosphenus japonicus)]** 277 AA

align

Score = 55.1 bits (131), Expect = 2e-06

Identities = 59/229 (25%), Positives = 87/229 (37%), Gaps = 53/229 (23%)

Query: 107 LPPNSELVQAVLRLRFQEPVP---KAALHR---HGRLSPRSAQARVTVEWLRVRDDGSNRT 160
 +P + A L +++E + +AALHR + L P +A DG+
 Sbjct: 3 IPDGEVITS AELHVYRERLSGPARAALHRINVYEVLRPAAA-----DGTPIA 49

Query: 161 SLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREHLGPLASGAHKLV 220
 L+D+R+V S W+ FDV+ A W + V+ HL + VR
 Sbjct: 50 RLLDTRVVHSGRSEWERFDVSPA AVRWAAARAPNHG---LLVEVHHLDGGTPEKRRHVR 105

Query: 221 F-----ASQGAPAGLGEPQLEL-----HTLDLRDYGAQGDCDPEA--- 255
 A +G G G PQL H RD G P+
 Sbjct: 106 IGRSLHAEAVAAAARDGAGEGGDGGEGWPQLRPLLVTFGHDGKTRDEGTLRPRPKRNSR 165

Query: 256 PMTEGTR----CCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCCQP 300
 P G R C R +Y+D + W +W++ PPG+ A+ C G C P
 Sbjct: 166 PNKGGRGRGRGCARYPLYVDFSDVGW-NDWIVAPPGYNFFCQGECHFP 213

tr O96504 **Bone morphogenetic protein 2/4 [AmphiBMP2/4] [Branchiostoma floridae (Florida lancelet) (Amphioxus)]** 361 AA

align

Score = 55.1 bits (131), Expect = 2e-06

Identities = 53/205 (25%), Positives = 83/205 (39%), Gaps = 17/205 (8%)

Query: 109 PNSSELVQAV-LRLRFQEPVPKAALHRHGRLSPRSAQARVTVEWLRV--RDDGSNRTSLIDS 165
 P+ EL++A LRLF+E + + ++G + E +R R + T L+D+
 Sbjct: 96 PSVELIKAAELRLRFREQIDVDHV-QYGDSTDHHLRVNVYEVMRPNSRTNTDTITRLLDT 154

Query: 166 RLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREHLGPLASGAHKLVRFASQG 225
 +LV V S W++FDV AV W V V G L++ +L R
 Sbjct: 155 KLVDVRNSSWESFDVRS AVTKWKNSPERNYGLE--VEVVS PKRGALSNHHVRLRRSTDM 212

Query: 226 APAGLGEPQLELHTLDLRDYGAQGDCDPEAPMTEGTR-----CCRQEMYIDLQGM 275
 + P L +T D + G + C R +Y+D +
 Sbjct: 213 DHSWQHRRPLLLLTYTDDGKGSSNSNRVASRQKRANGRKKQRRRLKANCRHSLYVDFSDV 272

Query: 276 KWAKNWWLEPPGFLAYECVGTCCQP 300
 W +W++ PPG+ AY C G C P
 Sbjct: 273 GW-NDWIVAPPGYQAYYCHGECFP 296

sp Q29607 **Bone morphogenetic protein 4 precursor (BMP-4) [BMP4]** 408
 BMP4_DAMDA [Dama dama
 (Fallow deer) (Cervus dama)] AA

align

Score = 54.3 bits (129), Expect = 3e-06

Identities = 56/227 (24%), Positives = 83/227 (35%), Gaps = 34/227 (14%)

Query: 92 SEASTHLLVFGMEQRLPPNSELVQAVLRLRFQEPVPKA-----ALHRHGRLSPRSAQARVT 146
 SE S +F + +P N + A LR F+E V + HR A
 Sbjct: 134 SENSAPFRFLFNLS--IPENQVISTAE LRDFREQVDQGPDWERGFHRINIYEVMPKPAEAV 191

Query: 147 VEWLVRVDDGSGNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXSVVQRE 206
 G T L+D+RLV + + W+ FDV+ AV W + V
 Sbjct: 192 -----PGHLITRLLDTRLVHHNVTRWETFDVSPAVLRW--TREKQPNYGLAIEVTHL 241

Query: 207 HLGPLASGAHKLVRFASQGAPAGLGE-----PQLELHTLDLRDYG-----AQGDGCDP 253
 H G H + S+ P G G+ P L D R + P
 Sbjct: 242 HQTRTHQGQHVRI---SRSLPQSGSDWAQLRPLLVTFGHDGRGHALTRHRRAKRSPKHHP 298

Query: 254 EAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQP 300
 + + C R +Y+D + W +W++ PPG+ A+ C G C P
 Sbjct: 299 QRARKKNKNCRRHSLYVDFSDVGW-NDWIVAPPGYQAFYCHGDCPFP 344

tr Q9U5E8 **Pf-BMP2/4 [Pf-bmp2/4] [Ptychodera flava]** 405 AA
align

Score = 54.3 bits (129), Expect = 3e-06
 Identities = 53/204 (25%), Positives = 86/204 (41%), Gaps = 14/204 (6%)

Query: 107 LPPNSELVQAVLRLRFQEPVPKAA--LHRHGRLSPRSAQARVTV-EWLVRVDDGSGNRTS-L 162
 +P N + A LRL+ + + ++ + R S R+ V E L D+G L
 Sbjct: 141 IPDNEVVTGAELRLYCQGINISSPMTNTDDRPEYQFLHRINVHEILEPADEGGESIKRL 200

Query: 163 IDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVS-VQREHLGPLASGAHKLVRF 221
 IDS++V + S W++FD+ AV W ++ VQ + P H +R
 Sbjct: 201 IDSKVVDIRNSSWESFDIRPAVAKWKASQEENHGVEVELTEVQNSQISPHKD--HVRLRR 258

Query: 222 ASQGAPAGLGE PQLELHTLDLRDYG AQGDGCDPEAPMTEGTR-----CCRQEMYIDLQGMK 276
 +S A A + Q L D + +G R C R+ +Y+D +
 Sbjct: 259 SSDLA-ASEWQRQRPLLITYTDDGKRPTRSKRNSERKKGGRKLKPNCRRRSLYVDFSDVG 317

Query: 277 WAKNWVLEPPGFLAYECVGTCQQP 300
 W +W++ PPG+ A+ C G C P
 Sbjct: 318 W-NDWIVAPPGYNAFYCDGECFP 340

sp O46564 **Bone morphogenetic protein 2 precursor (BMP-2) [BMP2]** 395
 BMP2_RABIT [Oryctolagus
 cuniculus (Rabbit)] AA
align

Score = 53.9 bits (128), Expect = 4e-06
 Identities = 51/216 (23%), Positives = 85/216 (38%), Gaps = 44/216 (20%)

Query: 107 LPPNSELVQAVLRLRFQEPVPKAA-----LHRHGRLSPRSAQARVTVEWLVRVDDGS 157
 +PP + A L++F+E + +A ++ + + P +A ++
 Sbjct: 138 IPPEEFITS AELQVFREQMQEALGDDSGFHHRINIYEIIKPATANSKFPA----- 187

Query: 158 NRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXSVVQREHLG-----PL 211
 T L+D+RLV+ + S W++FDVT AV W V+ E G +
 Sbjct: 188 --TRLLDTRLVNQNTSRWESFDVTPAVMRWTAQGHANHGFFVEVTHLEEKQGVSKRHVRI 245

Query: 212 ASGAHKLVRFASQGAPA-----GLGEPQLELHTLTLRLDYGAQGDCDPEAPMTEGTRCC 264
 + H SQ P G G P LH + R + + C
 Sbjct: 246 SRSLHPDEHSWSQIRPLLVTFGHDGKGHP---LHRREKR-----QAKHKQRKRLKSSCK 296

Query: 265 RQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300
 R +Y+D + W +W++ PPG+ A+ C G C P
 Sbjct: 297 RHPLYVDFSDVGW-NDWIVAPPGYHAFYCHGECPPF 331

sp O19006 **Bone morphogenetic protein 2 precursor (BMP-2) [BMP2]** 396
 BMP2_DAMDA [Dama dama AA
 (Fallow deer) (Cervus dama)] align

Score = 53.9 bits (128), Expect = 4e-06
 Identities = 52/216 (24%), Positives = 87/216 (40%), Gaps = 44/216 (20%)

Query: 107 LPPNSELVQAVLRLRFQEPVPKAAALHR---HGRLS-----PRSAQARVTVEWLRVRDDGS 157
 +P + A L++F + +P+A + H R++ P +A ++ V
 Sbjct: 139 IPTEEFITSaelQVFGKHMPEALENNSSFHHRINIFEI IKPATANSKFPV----- 188

Query: 158 NRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREHLGP-----L 211
 T L+D+RLV+ + S W++FDVT AV W V+ + G +
 Sbjct: 189 --TRLLDTRLVTQNASRWESFDVTPAVMRWTAQGLTNHGFVVEVAHPEDSYGASKRHRVRI 246

Query: 212 ASGAHKLVRFASQGAPA-----GLGEPQLELHTLTLRLDYGAQGDCDPEAPMTEGTRCC 264
 + H+ SQ P G G P LH + R + + C
 Sbjct: 247 SRSLHQDEHSWSQIRPLLVTFGHDGKGHP---LHRREKR-----QAKHKQRKRLKSSCK 297

Query: 265 RQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300
 R +Y+D + W +W++ PPG+ A+ C G C P
 Sbjct: 298 RHPLYVDFSDVGW-NDWIVAPPGYHAFYCHGECPPF 332

tr Q9PVK1 **Anti-dorsalizing morphogenetic protein [ADMP] [Gallus gallus 364 AA
 (Chicken)]** align

Score = 53.9 bits (128), Expect = 4e-06
 Identities = 57/208 (27%), Positives = 82/208 (39%), Gaps = 41/208 (19%)

Query: 123 EPVPKAAALHRHGRLSPRSAQARVTVEWLRV-----RDDGSNRTSLIDSRLVSVHES 173
 E + A LH RL PR+A+ + +V D L+ +RL+S+ S
 Sbjct: 102 EKILTAELHLF-RLWPRAAEGPRRHHCQVSVYQILDESEPDSPEGQKLLATRLLSLQGS 160

Query: 174 GWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREHLGPLASGAHKLVRFASQGAPAGLGEP 233
 GW+ F +T+AV W V LG A A V+FAS G +P
 Sbjct: 161 GWEVFAITQAVRDWTQDESSNRGLLVTV---HGLGGSALAE-PAVQFASSGDHSHSKP 215

Query: 234 QLELHTLTLRLDYGAQGDCDPEAPM-----TEGTR-----CCRQEMYIDL 272
 L L T D G +G P A + G R C R + +D
 Sbjct: 216 MLVLFT----DDGRRGASLPMAGVPASQPRDFPAKLSGPRARSRLDRLQPCQRHPLSVDF 271

Query: 273 QGMKWAKNWWLEPPGFLAYECVGTCQQP 300
 + + W+ W++ P G+ AY C G+C P

Sbjct: 272 EEIGWS-GWIIISPRGYNAYHCRGSCFPF 298

sp P30884 **Bone morphogenetic protein 2-II precursor (BMP-2-II)** 398
 BMPB_XENLA [**Xenopus** AA
laevis (African clawed frog)] align

Score = 53.1 bits (126), Expect = 8e-06
 Identities = 55/211 (26%), Positives = 89/211 (42%), Gaps = 37/211 (17%)

Query: 109 PNSELV-QAVLRLFQEPVVK-----AALHR---HGRLSPRSAQARVTVEWLRVRDDGSN 158
 P+ ELV + LR+F+E V + + LHR + + P +A +R V

Sbjct: 142 PDEELVTSSELRIIFREQVQEPFKTDGSKLHRINIYDIVKPAAAASRGPV----- 190

Query: 159 RTSLIDSRLVSVHESGWKAFDVT EAVNFWXXXXXXXXXXXXXSVQREHLGPLASGAHKL 218
 L+D+RL+ +ES W++FDVT A+ W V+ HL + +

Sbjct: 191 -VRLLDTRLIIHHNESKWESFDVTPAITRWIAHKQPNHGFVVEVT---HLDNDTNVPKRH 245

Query: 219 VRFASQGAPAGLGE-----PQLELHTLDLRDYGAQGDCDPEAPMTEGTR----CCRQEMY 269
 VR S+ G P L + D + + +A + R C R +Y

Sbjct: 246 VRI-SRSLTLDKGHWPRIRPLLVTFSHDGKGHALHKRQKRQARHKQKRKLKSSCRRHPLY 304

Query: 270 IDLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300
 +D + W +W++ PPG+ A+ C G C P

Sbjct: 305 VDFSDVGW-NDWIVAPPGYHAFYCHGECFPF 334

tr Q9VQG9 **CG16987-PA (Cg16987-pb) (GH14433p) [Alp23B]** 586 AA
 [Drosophila align
melanogaster (Fruit fly)]

Score = 53.1 bits (126), Expect = 8e-06
 Identities = 33/109 (30%), Positives = 53/109 (48%), Gaps = 20/109 (18%)

Query: 261 TRCCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQ---QPPEALAFNWPFL----- 311
 T CCR+ +YI + + W+ NW+L+P G+ AY C G+C +A + + +

Sbjct: 481 TECCREHLYISFRDIGWS-NWILKPEGYNAYFCRGSCSSVASVTQAASHHSSIMKILSTS 539

Query: 312 GPRQ-----CIASETASLPMIVSIKEGGRTRPQVVS LPMNRVQKSC 353
 G + C A + +SL ++V T V +LPNM V+ C C

Sbjct: 540 GANKSLELVPCCTAKQYSSLQLVMDSSNTAT---VKTLPMNVVESC GC 585

sp O08717 **Inhibin beta E chain precursor (Activin beta-E chain)** 350
 IHBE_MOUSE [**Inhbe**] [**Mus** AA
musculus (Mouse)] align

Score = 52.8 bits (125), Expect = 1e-05
 Identities = 33/121 (27%), Positives = 54/121 (44%), Gaps = 27/121 (22%)

Query: 251 CDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQ-----QPPEALA 305
 C+PE P+ CCR++ Y+D Q + W ++W+L+P G+ C G C P A +

Sbjct: 240 CEPETPL-----CCRRDHYVDFQELGW-RDWILQPEGYQLNYCSGQCPHLAGSPGIAAS 293

Query: 306 FN-----WPFLGPRQCIASETASLPMIVSIKEGGTRPQVVSLPNMRVQKCSC 353
F+ WP G C+ + L ++ G + V P+M V+ C C
Sbjct: 294 FHSVFSLLKANNPWP-AGSSCCVPTARRPLSLLYLDHNGNVVKTVDV---PDMVVEACGC 349

Query: 354 A 354
+
Sbjct: 350 S 350

sp P12643 Bone morphogenetic protein 2 precursor (BMP-2) (BMP-2A) 396
BMP2_HUMAN [BMP2] AA
[Homo sapiens (Human)] align

Score = 52.8 bits (125), Expect = 1e-05
Identities = 53/216 (24%), Positives = 86/216 (39%), Gaps = 44/216 (20%)

Query: 107 LPPNSELVQAVLRLFQEPVPKAAALHR---HGRLS-----PRSAQARVTVEWLRVRDDGS 157
+P + A L++F+E + A + H R++ P +A ++ V
Sbjct: 139 IPTEEFITS AELQVFREQMDALGNSSFHHRINIYEIIK PATANSKFPV----- 188

Query: 158 NRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREHLG-----PL 211
T L+D+RLV+ + S W++FDVT AV W V+ E G +
Sbjct: 189 --TRL DTRLVNQNASRWESFDVTPAVMRWTAQGHANHG FVVEVAHLEEKQGVSKRHVRI 246

Query: 212 ASGAHKLVRFASQGAPA-----GLGEPQLELHTLDLRDYGAQGDCDPEAPMTEGTRCC 264
+ H+ SQ P G G P LH + R + + C
Sbjct: 247 SRSLHQDEHSWSQIRPLLVTFGHDGKGHP---LHKREKR-----QAKHKQRKRLKSSCK 297

Query: 265 RQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300
R +Y+D + W +W++ PPG+ A+ C G C P
Sbjct: 298 RHPLYVDFSDVGW-NDWIVAPPGYHAFYCHGECPPF 332

tr Q91XH3 Inhibin beta E [Inhbe] [Mus musculus (Mouse)] 350 AA
align

Score = 52.8 bits (125), Expect = 1e-05
Identities = 33/121 (27%), Positives = 54/121 (44%), Gaps = 27/121 (22%)

Query: 251 CDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQ-----QPPEALA 305
C+PE P+ CCR++ Y+D Q + W ++W+L+P G+ C G C P A +
Sbjct: 240 CEPETPL-----CCRRDHYVDFQELGW-RDWILQPEGYQLNYCSGQCPPHLAGSPGIAAS 293

Query: 306 FN-----WPFLGPRQCIASETASLPMIVSIKEGGTRPQVVSLPNMRVQKCSC 353
F+ WP G C+ + L ++ G + V P+M V+ C C
Sbjct: 294 FHSVFSLLKANNPWP-AGSSCCVPTARRPLSLLYLDHNGNVVKTVDV---PDMVVEACGC 349

Query: 354 A 354
+
Sbjct: 350 S 350

tr Q7Q3Q7 **AgCP11289 (Fragment)** [agCG50272] [Anopheles gambiae str. PEST] 459 AA

align

Score = 52.8 bits (125), Expect = 1e-05

Identities = 81/367 (22%), Positives = 137/367 (37%), Gaps = 63/367 (17%)

```

Query: 41  PVLDRADMEKLVIPAHVRAQYVVLLRRS-----HGDRSRGKRFSQSFREVAGRFLA 91
           P  + D K+VIP ++ Y ++                      G +R      +SF
Sbjct: 101 PNRPKIDRSKVVPIEAMKQLYAQIMGHDLVDSVSPKEGLNTRNANTVRSFTHEESHIDQ 160

Query: 92  SEASTHL--LVFGMEQRLPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTVEW 149
           H  L+F +   +P  +L A L L +E +           HR R  R+      + +
Sbjct: 161 RFQHHHRFRLLFNVTS-IPRGEKLRAAELTLTREGIA----HRSSRAQARTPVLYQVMVY 215

Query: 150 LRVRRDGSNRTS----LIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXV---- 201
           VR      + +   L+D++ ++++ESG +FDV AV W                      V
Sbjct: 216 DIVRPGVKGKRAPTFLLVDTKTILAINESGTASFDMPAVERWLRQPRKNHGLFVQVTGRG 275

Query: 202  -----SVQREHLGPLASGAHKLVRFASQGAPAGLG----EPQLELHTLD-----LRD 244
           S QR  + P A  H+ VR      A          +P L  +T D          +RD
Sbjct: 276 RGPPGHSRQRRSIVP-AVPVHEHVRLRRNAAERHDSWVQKQPLLFTYTDDGRHKQRPIRD 334

Query: 245  YGAQGDCDPEAPMTEGTR-----CCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCCQ 299
           + +   A      +R      C R+ +Y+D  + W  +W++ PPG+ AY C G C+
Sbjct: 335 AISSANRARRASAKRSSRRKNELCQRKPLYVDFSDVGW-NDWIVAPPGYEAYYCQGDCRF 393

Query: 300  P-----PEALAFNW-PFLGPRQCIASETASLPMIVSIKEGGRTRPVVSLPNM 346
           P                      + L  ++ P L P+ C      S  ++ + E  + +  + + +M
Sbjct: 394 PIADHLNTTNHAIVQTLVNSYNPTLAPKACCVPTQLSSISMLYLNE--QNKVVLKNYQDM 451

Query: 347  RVQKCSC 353
           V  C  C
Sbjct: 452 TVVGCGC 458

```

tr Q6PUC6 **Decapentaplegic (Fragment)** [Anopheles gambiae (African malaria mosquito)] 379 AA

align

Score = 52.8 bits (125), Expect = 1e-05

Identities = 81/367 (22%), Positives = 137/367 (37%), Gaps = 63/367 (17%)

```

Query: 41  PVLDRADMEKLVIPAHVRAQYVVLLRRS-----HGDRSRGKRFSQSFREVAGRFLA 91
           P  + D K+VIP ++ Y ++                      G +R      +SF
Sbjct: 21  PNRPKIDRSKVVPIEAMKQLYAQIMGHDLVDSVSPKEGLNTRNANTVRSFTHEESHIDQ 80

Query: 92  SEASTHL--LVFGMEQRLPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTVEW 149
           H  L+F +   +P  +L A L L +E +           HR R  R+      + +
Sbjct: 81  RFQHHHRFRLLFNVTS-IPRGEKLRAAELTLTREGIA----HRSSRAQARTPVLYQVMVY 135

Query: 150 LRVRRDGSNRTS----LIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXV---- 201
           VR      + +   L+D++ ++++ESG +FDV AV W                      V
Sbjct: 136 DIVRPGVKGKRAPTFLLVDTKTILAINESGTASFDMPAVERWLRQPRKNHGLFVQVTGRG 195

Query: 202  -----SVQREHLGPLASGAHKLVRFASQGAPAGLG----EPQLELHTLD-----LRD 244
           S QR  + P A  H+ VR      A          +P L  +T D          +RD

```

Sbjct: 196 RGPPGHSRQRRSIVP-AVPVHEHVRLRRNAAERHDSWVQKQPLLFTYTDGGRHKQRPIRD 254

Query: 245 YGAQGDCDPEAPMTEGTR-----CCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQ 299
+ + A +R C R+ +Y+D + W +W++ PPG+ AY C G C+

Sbjct: 255 AISSANRARRASAKRSSRRKNELCQRKPLYVDFSDVGW-NDWIVAPPGYEAYYCQGD CRF 313

Query: 300 P-----PEALAFNW-PFLGPRQCIASETASLPMIVSIKEGGRTRPQVVSLPNM 346
P + L ++ P L P+ C S ++ + E + + + + +M

Sbjct: 314 PIADHLNTTNHAIVQTLVNSYNPTLAPKACCVPTQLSSISM LYLNE--QNKVVLKNYQDM 371

Query: 347 RVQKCSC 353
V C C

Sbjct: 372 TVVGCGC 378

tr Q9W6T9 **Activin beta B protein (Fragment) [inhbb] [Brachydanio rerio 138 AA
(Zebrafish) (Danio rerio)]**

align

Score = 52.0 bits (123), Expect = 2e-05

Identities = 37/140 (26%), Positives = 62/140 (43%), Gaps = 25/140 (17%)

Query: 231 GEPQLELHTLDRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWWLEPPGFLA 290
G QL+L L + G+ +CD G CCRQ+ YID + + W +W++ P G+

Sbjct: 1 GLEQLKLACLQVDSRSGSFEC DGN---NGGLCCRQQFYIDFRLIGW-NDWIIAPAGYYG 55

Query: 291 YECVGTCQQ-----PPEALAFNWPFLGPRQ-----CIASETASLPMIVSIKEG 333
C G+C P A +F+ + + CI ++ +++ M+ E

Sbjct: 56 NYCEGSCPAYMAGVPGSASSFHTAVVNQYRMRGMSPGSVNSCCIPTKLSTMSMLYFDDEY 115

Query: 334 GRTRPQVVSLPNMRVQKCSC 353
+ V PNM V++C C

Sbjct: 116 NIVKRDV---PNMIVEECGC 132

tr Q9PWR8 **Activin beta B subunit precursor [Carassius auratus
(Goldfish)]**

392

AA

align

Score = 52.0 bits (123), Expect = 2e-05

Identities = 79/353 (22%), Positives = 131/353 (36%), Gaps = 66/353 (18%)

Query: 42 VLDRADMEKLVIPAHV--RAQYVLLRRSHGDRSR--GKRFSQSFREVAGRFLASEASTH 97
+L+R M + H +A V LR+ H + R G+ +F A E ++

Sbjct: 66 ILNRLQMRERPNI THPIPKAAMVTALRKLHAGKVREDGRVEIPNFDGHA AHNEVQEETSE 125

Query: 98 LLVFGMEQRLPPNSELVQAVLRLFQEP---VPK AALHRHGRLSP---RSAQARVTVEWL 150
++ F + P+ + ++ V +A L + +L P + + +VTV

Sbjct: 126 IISFAESDDVTPSKSSLYFLISNEGNQNLVYLQANLWLYFKLLPGTQEKGLRRKVTVRVR 185

Query: 151 RVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXSVSQREHLGP 210
G N + + V + SGW F V+EAV RE L

Sbjct: 186 SYEPGGQNVHWPMM EKRVELKRSGWHTFPVSEAV-----REMLAK 225

Query: 211 LASGAHKLVRFASQGAPAG-----LGEPQLELHTLDRDYGAQGDCDP-----EAPMT 258

```
      G  + +      +G A      L +P      H  L      Q D      E  T
Sbjct: 226 --GGRRQDLDIHCEGCEAANVLPILVDPSPDPSHRPFLVVRAQQADSKHRIRKRGLECDGT 283

Query: 259 EGTRCCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQ-----PPEALAFNWPFLGP 313
      G  CCRQ+ YID + + W  +W++ P G+      C G+C      P  A +F+  +
Sbjct: 284 NGGLCCRQQFYIDFRLIGW-NDWIIAPAGYYGNYCEGSCPAYMAGVPGSASSFHTAVVNQ 342

Query: 314 RQ-----CIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSA 354
      +      CI ++ +++ M+      E      + V      PNM V++C CA
Sbjct: 343 YRMGISPGSVNSCCIPTKLSTMSMLYFDDEYNIVKRDV--PNMIVEECGCA 392
```

tr Q869H8 **GDF2 precursor [Crassostrea gigas (Pacific oyster)]** 387 AA
align

Score = 52.0 bits (123), Expect = 2e-05
Identities = 49/217 (22%), Positives = 85/217 (38%), Gaps = 31/217 (14%)

```
Query: 161 SLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXSVQREHLGPLASGAHKLVR 220
      +L++SR + +      GW+ FD+T+ V  W      + V      G L  + +
Sbjct: 179 TLVESRTIDLSRDGWEIFDITQDVQDWIEDPELNNGIE--IFVDGLDAGQLVFPSLNITE 236

Query: 221 FASQGAPAGLGEPQLELHTLDRDYGA-----QGDCDP-EAPMTEG-TRCCRQEMYI 270
      S  +      P + L  L+++ +      Q D +  +      +G +RCCR  I
Sbjct: 237 RMSSKSSTNTTIPNVILPILEMKTHERSILKRVKRQNDIERRDCVKGDGESRCCRFTTTI 296

Query: 271 DLQGMKWAKNWWLEPPGFLAYECVGTCQQPPEALAFNWPFLG-----PRQCI 317
      + W  +W+L PP + A+ C G+C  P+      F G      P+ C
Sbjct: 297 AFSDLGW-NDWILAPPDYEAHYCDGSC---PDRFKMANTFAGIQARLHALYPNKFPPKCC 352

Query: 318 ASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSA 354
      S P+ +  K+      + Q+  P+M V+ C CA
Sbjct: 353 VPSKLS-PLTILHKDSS-GKYQLTDYPDMIVEDCKCA 387
```

tr Q8MKC2 **Bone morphogenetic protein 2 (Fragment) [Ovis aries (Sheep)]** 223 AA
align

Score = 51.6 bits (122), Expect = 2e-05
Identities = 41/154 (26%), Positives = 63/154 (40%), Gaps = 23/154 (14%)

```
Query: 160 TSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXSVQREHLGP-----LAS 213
      T L+D+RLV+ + S W++FDVT AV  W      V+  + G      ++
Sbjct: 42  TRLLDTRLVTQNASRWESFDVTPAVMRWTAQGLTNHGFVVEVAHPEDSHGASKRHVRISR 101

Query: 214 GAHKLVRFASQGAPA-----GLGEPQLELHTLDRDYGAQGDCDPEAPMTEGTRCCRQ 266
      H+      SQ  P      G G P  LH  + R      +      + C R
Sbjct: 102 SLHQDEHSWSQIRPLLVTFGHDGKGHP---LHRREKR-----QAKHKQRKRLKSSCKRH 152

Query: 267 EMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300
      +Y+D  + W  +W++ PPG+ A+ C G C  P
Sbjct: 153 PLYVDFSDVGW-NDWIVAPPGYHAFYCHGECPPF 185
```

tr Q8IAE3 **Sj-BMP2/4 [Sj-bmp2/4] [Stichopus japonicus (Sea cucumber)]** 422 AA

align

Score = 51.2 bits (121), Expect = 3e-05

Identities = 62/250 (24%), Positives = 94/250 (36%), Gaps = 30/250 (12%)

Query: 80 QSFREVAGRFLASEA-STHLLVFGMEQRLPPNSELVQAVLRLRFQEPVP-----KAALHR 132

+SF + F EA H LVF + + L A LRLF+ +P + AL+

Sbjct: 118 KSFHHIEEHFDIDEAIHRHRLVFNLS-IENEEILTAAELRLFRHAIPDHKIRKRHALNE 176

Query: 133 HGRLSPRSAQARVTVEWLRVRDDGSNRT---SLIDSRLVSVHESGWKAFDVTEAVNFWXX 189

++ R+ + + ++ NR LIDS ++ V + W++ DV AV W

Sbjct: 177 SENITDGKVIQRINLYQI-LKPVARNRDVIKRLIDSIVIDVRNTTWESLDVAPAVKSWTN 235

Query: 190 XXXXXXXXXXXXSVQREHLGPLASGAHKLVRFA SQGAPAGLG-----EPQLELHT 239

+ +R P G L G A L P L +T

Sbjct: 236 DANSNYGVEIEIIDRRG--SPSRHGDDHLRTRRRIGDDASLEIHDEDQWFQQRPLLVITYT 293

Query: 240 LDLRDYGAQGDCDPEAPMTEGTR----CCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVG 295

D R + + R C + +Y+D + W +W+L P G+ AY C G

Sbjct: 294 DDGRTKRSSKKRTKRQSKKKRRLKENCSKHSLYVDFAIVGW-DSWILAPEGYQAYYCQG 352

Query: 296 TCQQP-PEAL 304

C P PE L

Sbjct: 353 ECPYPMPEHL 362

tr Q6XDQ0 **Bone morphogenetic protein 2 [Gallus gallus (Chicken)]** 392 AA
align

Score = 50.4 bits (119), Expect = 5e-05

Identities = 57/213 (26%), Positives = 86/213 (39%), Gaps = 41/213 (19%)

Query: 109 PNSELV-QAVLRLRFQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNR---TSLID 164

PN E V A L++F+E V +A S S R+ + + +++ T L+D

Sbjct: 136 PNEESVTSaelQIFREQVHEAFE-----SNSSYHHRINIYEIMKPATATSKDPVTRLID 189

Query: 165 SRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXXSVQREHLGPLASGAHKLVRFA-- 222

+RLV + S W++FDVT AV W V+ HL S + + VR +

Sbjct: 190 TRLVHHNASKWESFDVTPAVLRWIAHGQPNHGFV----VEVVHLDKENSASKRHRVRSRS 245

Query: 223 -----SQGAPA-----GLGEPQLELHTLDLRDYGAQGDCDPEAPMTEGTRCCRQE 267

SQ P G G P LH + R + C R

Sbjct: 246 LHQDEDSWSQLRPLLVTFGHDGKGHP---LHKREKRQ-----AKHKQRKRHKYSCKRHP 296

Query: 268 MYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300

+Y+D + W +W++ PPG+ A+ C G C P

Sbjct: 297 LYVDFNDVGW-NDWIVAPPGYSAFYCHGECPPF 328

sp P27093 **Inhibin beta B chain precursor (Activin beta-B chain)** 391
IHBB_CHICK **[INHBB]** AA

[Gallus gallus (Chicken)]

align

Score = 50.1 bits (118), Expect = 6e-05

tr O13109 **BMP2 [bmp2a] [Brachydanio rerio (Zebrafish) (Danio rerio)]** 386 AA

align

Score = 50.1 bits (118), Expect = 6e-05

Identities = 68/252 (26%), Positives = 102/252 (39%), Gaps = 47/252 (18%)

Query: 65 LRRSHGDRSRGKRFSQSFEVAGRFLASEASTHLLVFGMEQRLPPNSELV-QAVLRLFQE 123
+R H D S S S R RFL + S P+ ELV A +R+F+E

Sbjct: 102 IRSFHHDESTEDPSSSSVRTTQ-RFLFNLTISI-----PDEELVTSADVRVFRE 148

Query: 124 PVPKAALHRHGRSLSPRSAQA-RVTVEWLRVRDDGSGNR---TSLIDSRLVSVHESGWKAFD 179
+ + L+ SA R+ V +R GS + T L+D+RLV S W++FD

Sbjct: 149 QIVSS-----LNNASAGFHRINVHEI-IRPSGSLQEPITRLLDTRLVQHSLSKWESFD 200

Query: 180 VTEAVNFWXXXXXXXXXXXXXVSV---QREHLGPLASGAHKLVRFASQGAPA----- 228
VT AV W +S R+H+ ++ H SQ P

Sbjct: 201 VTPAVLKWTTDGHPNHGILVEISHPDQDSRKHVR-VSRSLHNNEDTWSQMRPLLVTYSHD 259

Query: 229 GLGEPQLELHTLDLRDYGAQGDCDEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGF 288
G G LH+ + R + + C R +Y+D + W +W++ PPG+

Sbjct: 260 GKGNV---LHSREKRQAR-----NNKQRKKHKANCRRHSLYVDFSDVGW-NDWIVAPPGY 310

Query: 289 LAYECVGTCQQP 300

A+ C G C P

Sbjct: 311 HAFYCQGECPFP 322

sp O88959 **Inhibin beta E chain precursor (Activin beta-E chain)** 350

IHBE_RAT [Inhbe]

[Rattus norvegicus (Rat)]

AA

align

Score = 49.7 bits (117), Expect = 8e-05

Identities = 32/121 (26%), Positives = 53/121 (43%), Gaps = 27/121 (22%)

Query: 251 CDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGF LAYECVGTCQ-----QPPEALA 305
C+ E P+ CCR++ Y+D Q + W ++W+L+P G+ C G C P A +

Sbjct: 240 CESETPL-----CCRRDHYVDFQELGW-RDWILQPEGYQLNYCSGQCPPHLAGSPGIAAS 293

Query: 306 FN-----WPFLGPRQCIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSC 353
F+ WP G C+ + L ++ G + V P+M V+ C C

Sbjct: 294 FHSAVFSLLKANNPWP-AGSSCCVPTARRPLSLLYLDHNGNVVKTDV---PDMVVEACGC 349

Query: 354 A 354

+

Sbjct: 350 S 350

sp P17491 **Inhibin beta B chain precursor (Activin beta-B chain)** 411

IHBB_RAT [Inhbb]

[Rattus norvegicus (Rat)]

AA

align

Score = 49.7 bits (117), Expect = 8e-05

Identities = 69/291 (23%), Positives = 117/291 (39%), Gaps = 45/291 (15%)

```

Query: 81 SFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKAAALHRHGRLSPRS 140
      SF E G LAS S L F + N +VQA L L+ + +P +
Sbjct: 149 SFAETDG--LAS--SRVRLYFFVSNEGNQNLFFVQASLWLYLKLLPYVL-----EKG 196

Query: 141 AQARVTVEWLRVRDDGNSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXX 200
      ++ +V V+ +R ++++ + V + SGW F +TEA+
Sbjct: 197 SRRKVRVKVYFQEQQHGDWRNVVEKK-VDLKRSWHTFPITEAIQ----ALFERGERRLN 251

Query: 201 VSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDRDYGAQGDCDPEAPMTEG 260
      + VQ + LA + P + + +L +R G + CD +
Sbjct: 252 LDVQCDSCQELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLE--CDGRTSL--- 306

Query: 261 TRCCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQ-----PPEALAFNWPFL---- 311
      CCRQ+ +ID + + W +W++ P G+ C G+C P A +F+ +
Sbjct: 307 --CCRQQFFIDFRLIGW-NDWIIAPTGYGYNYCEGSCPAYLAGVPGSASSFHTAVVNQYR 363

Query: 312 -----GPRQ--CIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSA 354
      GP CI ++ +S+ M+ E + V PNM V++C CA
Sbjct: 364 MRGLNPGPVNSCCIPTKLSSMSMLYFDDEYNIVKRDV---PNMIVEECGCA 411

```

```

sp Q04999      Inhibin beta B chain precursor (Activin beta-B chain)      367
IHBB_MOUSE    (Fragment)                                                  AA
               [Inhbb] [Mus musculus (Mouse)]                             align

```

Score = 49.7 bits (117), Expect = 8e-05

Identities = 69/291 (23%), Positives = 117/291 (39%), Gaps = 45/291 (15%)

```

Query: 81 SFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKAAALHRHGRLSPRS 140
      SF E G LAS S L F + N +VQA L L+ + +P +
Sbjct: 105 SFAETDG--LAS--SRVRLYFFVSNEGNQNLFFVQASLWLYLKLLPYVL-----EKG 152

Query: 141 AQARVTVEWLRVRDDGNSNRTSLIDSRLVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXXXXX 200
      ++ +V V+ +R ++++ + V + SGW F +TEA+
Sbjct: 153 SRRKVRVKVYFQEQQHGDWRNVVEKK-VDLKRSWHTFPITEAIQ----ALFERGERRLN 207

Query: 201 VSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDRDYGAQGDCDPEAPMTEG 260
      + VQ + LA + P + + +L +R G + CD +
Sbjct: 208 LDVQCDSCQELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLE--CDGRTSL--- 262

Query: 261 TRCCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQ-----PPEALAFNWPFL---- 311
      CCRQ+ +ID + + W +W++ P G+ C G+C P A +F+ +
Sbjct: 263 --CCRQQFFIDFRLIGW-NDWIIAPTGYGYNYCEGSCPAYLAGVPGSASSFHTAVVNQYR 319

Query: 312 -----GPRQ--CIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSA 354
      GP CI ++ +S+ M+ E + V PNM V++C CA
Sbjct: 320 MRGLNPGPVNSCCIPTKLSSMSMLYFDDEYNIVKRDV---PNMIVEECGCA 367

```

```

sp O95393      Bone morphogenetic protein 10 precursor (BMP-10) [BMP10]    424
BM10_HUMAN    [Homo                                                         AA
               sapiens (Human)]                                             align

```

Score = 49.7 bits (117), Expect = 8e-05
Identities = 50/235 (21%), Positives = 88/235 (37%), Gaps = 50/235 (21%)

Query: 107 LPPNSELVQAVLRLRFQEPVPKAAALHRHGRLSPRSAQARVTV-EWLRVRDDGS---NRTSL 162
+P + E++ A LRL+ L + R+ ++T+ E L + D N L
Sbjct: 134 IPHHEEVIMAELRLY-----TLVQRDRMIYDGVDRKITIFEVLESKGDNEGERNMLVL 186

Query: 163 IDSRLVSVHESGWKAFDVTAVNFVXXXXXXXXXXXXXSVQREHLGPIASGAHK----- 217
+ + + S W+ FDVT+A+ W + + + +SG +
Sbjct: 187 VSGEIYGTN-SEWETFDVTDAIRRWQKSGSSTHQLEVHIESKHDEAEDASSGRLEIDTSA 245

Query: 218 -----LVRFASQGAPAGLGEPQL-----ELHTLDRDYGAQGDCDPEAPM--- 257
L+ F+ + +L EL L L + + + M
Sbjct: 246 QNKHNPLLVFSDQSSDKERKEELNEMISHEQLPELDNLGLDSFSSGPGEALLQMRSN 305

Query: 258 -----TEGTRCCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300
+G C R +YID + + W +W++ PPG+ AYEC G C P
Sbjct: 306 IIYDSTARIRRNAKGNKYCKRTPLYIDFKEIGW-DSWIIAPPGYEAYECRGVCNYP 359

sp P48969 **DVR-1 protein homolog precursor [DVR1] [Strongylocentrotus** 461 AA
DVR1_STRPU purpuratus (Purple sea urchin)]
[align](#)

Score = 49.3 bits (116), Expect = 1e-04
Identities = 50/226 (22%), Positives = 88/226 (38%), Gaps = 49/226 (21%)

Query: 106 RLPPNSELVQAVLRLRFQEPVPKAAALHRHGRLSPRSAQARVTVEWLRVR-DDGSNRTSLID 164
R+P + A LR+F++ R GR + R+ V LR R DGS +D
Sbjct: 189 RIPQGETVTSaelrvfrda-----GRQGR-----SLYRIDVLLLREGRSDGSRSPVYLD 237

Query: 165 SRLVSVHESGWKAFDVTAVNFVXXXXXXXXXXXXXSVQREHLGP----- 210
S +V + GW FD+T A + W V S+Q ++ P
Sbjct: 238 STIVGAGDHGWLVDMTSATSTWRSYPGANVGLQLRVESLQGLNIDPTDAGVVGVGNNNEG 297

Query: 211 -----LASGAH-KLVRFASQGAPAGLGEPQLELHTLDRDYGAQGDCDPE 254
+A+ +H + R A+ G P+ D+ D
Sbjct: 298 REPFMVVFFQRNEEVIATNSHLRRNRRAATRQKKGKRPKPDNDI-----ASRDSA 351

Query: 255 APMTEGTRCCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300
+ + +C R+ +++ + + W + W++ P G++A+ C G C P
Sbjct: 352 SSLNSDWQCKRKNLFVNFEDLDW-QEWIIAPLG YVAFYCQGECAFP 396

tr Q90261 **Activin beta B [inhbb] [Brachydanio rerio (Zebrafish) (Danio** 393 AA
rerio)]
[align](#)

Score = 49.3 bits (116), Expect = 1e-04
Identities = 59/249 (23%), Positives = 94/249 (37%), Gaps = 63/249 (25%)

Query: 139 RSAQARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTAVNFVXXXXXXXXXXXXX 198
+ +A+VTV G N + + V + SGW F V+EA+
Sbjct: 175 KGLRAKVTVRVHSYEPGGQNVHWPMEKRVELKRSWHTFPVSEAI----- 220

Query: 199 XXVSVQREHLGPLASGAHKLVRFASQGAPAG-----LGEPQLELHT--LDLRDYGAQG-- 249
 RE L G + + +G A L +P H L +R A G
 Sbjct: 221 -----REMLAK--GGRRQDLDIHCEGCEANVLPILVDPSPDPSHRPFLVVRAQQADGKH 272

Query: 250 -----DCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQ--- 299
 +CD G CCRQ+ YID + + W +W++ P G+ C G+C
 Sbjct: 273 RIRKRGLECDGN----NGGLCCRQQFYIDFRLIGW--NDWIIAPAGYYGNYCEGSCPAYMA 327

Query: 300 --PPEALAFNWPFLGPRQ-----CIASETASLPMIVSIKEGGRTRPQVVSLPN 345
 P A +F+ + + CI ++ +++ M+ E + V PN
 Sbjct: 328 GVPGSASSFHTAVVNQYRMGMSPGSVNSCCIPTKLSTMSMLYFDDEYNIVKRDV---PN 384

Query: 346 MRVQKCSA 354
 M V++C CA
 Sbjct: 385 MIVEECGCA 393

tr Q869H7 **GDF3 precursor (Fragment) [Crassostrea gigas (Pacific oyster)]** 251 AA

align

Score = 49.3 bits (116), Expect = 1e-04

Identities = 56/238 (23%), Positives = 95/238 (39%), Gaps = 57/238 (23%)

Query: 162 LIDSRLVSVHESGWKAFDVTAVNFVXXXXXXXXXXXXXV-----SVQREHLGPLASGAH 216
 +ID++ V +SGW+ FDVT AV W + SV L L H
 Sbjct: 24 VIDTQHVIYGRDSGWETFVDVTSAVRRVWTKPSSSQILEIRIESVFHSVTDGDLDFLTPEQH 83

Query: 217 K----LVRFASQGAPAGLGEPQLELHTLDLRDYGAQGDC--DPEAPMT----- 258
 K LV F++ + +L+LH + + + D D ++P++
 Sbjct: 84 KNEPLLTVFSTD-----KQKLQLHKTERHELITREDSIYDIQSPLSGSKNSNNSLNET 136

Query: 259 -----EGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQPP 301
 G C R+ M ++ ++W +W+L P + AYECVG C P
 Sbjct: 137 NTIGHKIHSRVKRRGRSGGLCRRRPMTVNFADIQW--DSWILAPSSYEAYECVGKCHFPV 195

Query: 302 E---ALAFNWPFLGPRQ--CIASETASLPMIVSIKEGGRT-RPQVVSLPNMRVQKCSA 353
 + + P PR+ C+ ++ S+ ++ + G T +P+ M V +C C
 Sbjct: 196 NERLSPSLTMPKEYPRESCCVPTKLDSISILYYDEYGVLTYPKPK--YDGMVVTECGC 250

sp P09529 **Inhibin beta B chain precursor (Activin beta-B chain)** 407

IHBB_HUMAN [INHBB] [Homo

AA

sapiens (Human)]

align

Score = 48.5 bits (114), Expect = 2e-04

Identities = 67/291 (23%), Positives = 116/291 (39%), Gaps = 45/291 (15%)

Query: 81 SFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKAAALHRHGRLSPRS 140
 SF E G LAS S L F + N +VQA L L+ + +P +
 Sbjct: 145 SFAETDG--LAS--SRVRLYFFISNEGNQNLFFVQASLWLYLKLLPYVL-----EKG 192

Query: 141 AQARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTAVNFVXXXXXXXXXXXXX 200
 ++ +V V+ +R ++++ R V + SGW F +TEA+
 Sbjct: 193 SRRKVRVKVYFQEQGHGDRWNMVEKR--VDLKRSGWHTFPLTEAIQ----ALFERGERRLN 247

Query: 201 VSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDRDYGAQGDCDPEAPMTEG 260
 + VQ + LA + P + + +L +R G + CD +
 Sbjct: 248 LDVQCDSCQELAVVPVFVDPEESHRRPFVVVQARLGDSRHRIRKRGLE--CDGRTNL--- 302

Query: 261 TRCCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQ-----PPEALAFNWPFLGPRQ 315
 CCRQ+ +ID + + W +W++ P G+ C G+C P A +F+ + +
 Sbjct: 303 --CCRQQFFIDFRLIGW-NDWIIAPTGYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYR 359

Query: 316 -----CIASETASLPMIVSIKEGGRTRPQVVSPLPNMRVQKSCA 354
 CI ++ +++ M+ E + V PNM V++C CA
 Sbjct: 360 MRGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDV---PNMIVEECGCA 407

tr Q9PTF9 **Bone morphogenetic protein 7 [bmp7] [Brachydanio rerio** 432
(Zebrafish) AA
(Danio rerio)] align

Score = 48.5 bits (114), Expect = 2e-04
 Identities = 46/173 (26%), Positives = 66/173 (37%), Gaps = 44/173 (25%)

Query: 162 LIDSRVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXSVSVQR----- 205
 L+DSR+V E GW FD+T N W V
 Sbjct: 205 LLDSRVVWAAEEGWLVDLTVTSNHWVINPGQNLGLQLLVETSHGARMNPRRAGLVGSSG 264

Query: 206 -EHLGPL-----ASGAH-KLVRFASQG-----APAGLGEPQLELHTLDRDYGA 247
 ++ P ASG H + VR AS G A G Q+ L T + + GA
 Sbjct: 265 AQNKQPFMVAFLKASGIHLRSVRSASGGKQKGHRRTKNAKPGAHSQVALKTAEATE-GA 323

Query: 248 QGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300
 DP+ C + E+Y+ + + W ++W++ P G+ AY C G C P
 Sbjct: 324 S--IDPKQG-----CKKHELYVSFRDLGW-QDWIIAPEGYAAYYCEGECVFP 367

tr Q6EH35 **Bone morphogenetic protein 2 (Fragment) [BMP-2] [Trachemys** 285
scripta AA
(Red-eared slider turtle) (Pseudemys scripta)] align

Score = 48.5 bits (114), Expect = 2e-04
 Identities = 51/207 (24%), Positives = 83/207 (39%), Gaps = 29/207 (14%)

Query: 109 PNSE-LVQAVLRLRFQEPVPKAAALHRHGRSLSPRSQAQARVTVEWLRVRDDGSNRTSLIDSRL 167
 PN E L A L++F+E V + + + +D + L+D+RL
 Sbjct: 33 PNEEFLTSAELQIFREQVQETFENNSSYHHRINIYEIIEAATATSKDPAAR---LLDTRL 89

Query: 168 VSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXV-----SVQREHLGPLASGAHKLVR 220
 V + S W++FDVT AV W V SV + H+ ++ H+
 Sbjct: 90 VHQNASKWESFDVTPAVMRWIAHRQPNHGFIIVEVHLDNESSVSKRHVR-ISRSLHQDED 148

Query: 221 FASQGAPA-----GLGEPQLELHTLDRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQ 273
 SQ P G G H+L R+ + + + C R +Y+D
 Sbjct: 149 SWSQLRPLLVTFGHDGKG-----HSLHKRE---KRQAKHKQRKRHKSSCKRHPYVDFN 199

Query: 274 GMKWAKNWWLEPPGFLAYECVGTCQQP 300
 + W +W++ PPG+ A+ C G C P

Sbjct: 200 DVGW-NDWIVAPPGYGAFYCHGECFPF 225

sp P58166 **Inhibin beta E chain precursor (Activin beta-E chain)** 350
IHBE_HUMAN [INHBE] [Homo
sapiens (Human)] AA
align

Score = 48.1 bits (113), Expect = 2e-04
Identities = 31/121 (25%), Positives = 52/121 (42%), Gaps = 27/121 (22%)

Query: 251 CDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQ-----QPPEALA 305
C+P P+ CCR++ Y+D Q + W ++W+L+P G+ C G C P A +
Sbjct: 240 CEPATPL-----CCRRDHYVDFQELGW-RDWILQPEGYQLNYCSGQCPPHLAGSPGIAAS 293

Query: 306 FN-----WPFLGPRQCIASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSC 353
F+ WP C+ + L ++ G + V P+M V+ C C
Sbjct: 294 FHSAVFSLKANNPWP-ASTSCCVPTARRPLSLLYLDHNGNVVKTDV---PDMVVEACGC 349

Query: 354 A 354
+
Sbjct: 350 S 350

sp Q9R229 **Bone morphogenetic protein 10 precursor (BMP-10) [Bmp10]** 420
BM10_MOUSE [Mus
musculus (Mouse)] AA
align

Score = 48.1 bits (113), Expect = 2e-04
Identities = 57/234 (24%), Positives = 89/234 (37%), Gaps = 51/234 (21%)

Query: 107 LPPNSELVQAVLRLRFQEPVPKAAALHRHGRLSPRSAQARVTVEWLRVRDDGSN--RTSLID 164
+P + E+V A LRL+ L + R+ ++T+ + DGS R+ L+
Sbjct: 133 IPHHEEVVMAELRLY-----TLVQRDRMMYDGVDRKITIFEVLESADGSEEERSMLV- 184

Query: 165 SRLVSVH----ESGWKAFDVT EAVNFWXXXXXXXXXXXXXXXXXSVQREHLGPLASGAHK--- 217
LVS S W+ FDVT+A W + ++ G +
Sbjct: 185 --LVSTEIYGTNSEWETFDVTDATRRWQKSGPSTHQL EIHIESRQNAEDTGRGQLEIDM 242

Query: 218 -----LVRFASQGAPAGLGEPQL-ELHT----LDLRDYGAQGDCDPEAPM----- 257
LV F+ + + +L EL T LDL D EA +
Sbjct: 243 SAQNKHDPLLVVFSDDQSNKEQKEELNELITHEQDLDLDSDAFFSGPDEEALLQMRNM 302

Query: 258 -----TEGTRCCRQEMYIDLQGMKWAKNWWLEPPGFLAYECVGTCQQP 300
+G C + +YID + + W +W++ PPG+ AYEC G C P
Sbjct: 303 IDDSSTRIRRNAKGNYCKKTPLYIDFKEIGW-DSWIIAPPGYEAYECRGVCNYP 355

sp Q24735 **60A protein precursor (Glass bottom boat protein) [gbb]** 436
60A_DROVI [Drosophila
virilis (Fruit fly)] AA
align

Score = 48.1 bits (113), Expect = 2e-04
Identities = 60/283 (21%), Positives = 103/283 (36%), Gaps = 47/283 (16%)

```

Query: 107 LPPNSELVQAVLRLRFQEPVPKAAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRTSLIDSR 166
      +P ++ L+ A LR++Q          G+ + + Q VTV LR      N      + S
Sbjct: 164 IPTDNYLMMAELRIYQNS-----NEGKWTNTNKQFTVTVMYLRSGGSAPNMLEPLSSV 216

Query: 167 LVSVHESGWKAFDVTEAVNFWXXXXXXXXXXXXXVSV----QREHLGPLASGAHKLVRF 222
      +      GW      +VTEA++ W          +RE          H+ +
Sbjct: 217 NTTGDYVGWLELNVTEALHDWRVNSNENHGIYIGAHALNKPEREIKLDDIGLIHRRTKVD 276

Query: 223 SQGAPAGLG-----EPQLELHTLTLRDYGAQGDCDPEAPMT-EGTRCCR 265
      + P +G          + + + TL R          +P      + E TR C+
Sbjct: 277 DENQPFMIGFFRGPPELIKSTSGHSTQKRTKRSTLHQRKKSSEPVNPFIENTRSCQ 336

Query: 266 -QEMYIDLQGMKWAKNWNVLEPPGFLAYECVGTCQQPPEA-----LAFNWPFL 311
      Q +YID + + W      +W++ P G+ A+ C G C P A          + P
Sbjct: 337 MQTLYIDFKDLGW-HDWIIAPEGYGAFYCSGECNFPLNAHMNATNHAIVQTLVHLLPEPKR 395

Query: 312 GPRQCIA-SETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSC 353
      P+ C A +      +LP++ + +          +      NM V+ C C
Sbjct: 396 VPKPCCAPTRLGALPVLYHLND---ENVNLKKYRNMIVKSCGC 435

```

tr Q9DGF1 **Inhibin/activin (Fragment) [Cyprinus carpio (Common carp)]** 115 AA

align

Score = 48.1 bits (113), Expect = 2e-04
 Identities = 31/117 (26%), Positives = 52/117 (43%), Gaps = 21/117 (17%)

```

Query: 254 EAPMTEGTRCCRQEMYIDLQGMKWAKNWNVLEPPGFLAYECVGTCQQ-----PPEALAFNW 308
      E   T G   CCRQ+ YID + + W      +W++ P G+      C G+C          P A +F+
Sbjct: 3   ECDGTNGGLCCCRQQFYIDFRLIGW-NDWIIAPAGYYGNYCEGSCPAYMAGVPGSASSFHT 61

Query: 309 PFLGPRQ-----CIASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSC 353
      +   +          CI ++ +++ M+      E      + V      PNM V++C C
Sbjct: 62  AVVNQYRMRGMSPGSVNSCCIPTKLSTMSMLYFDDEYNIVKRDV---PNMIVEECGC 115

```

Database: EXPASY/UniProt

Posted date: Nov 8, 2004 3:52 PM

Number of letters in database: 518,174,383

Number of sequences in database: 1,621,919

Lambda	K	H
0.322	0.136	0.436

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

length of query: 366

length of database: 518,174,383

effective HSP length: 126

effective length of query: 240
effective length of database: 313,812,589
effective search space: 75315021360
effective search space used: 75315021360
T: 11
A: 40
X1: 16 (7.4 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.9 bits)
S2: 74 (33.1 bits)

 ExPASy Home page	Site Map	Search ExPASy	Contact us	Proteomics tools	Swiss-Prot
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CLUSTAL W (1.74) multiple sequence alignment

```

sp|O00292|TGF4_HUMAN      MWPLWLCWALWVLPPLAGPGAALTEEQLLGSLLRQLQLSEVPVLDRADMEKLVIPAHVRA
sp|O75610|LFTB_HUMAN      MQPLWLCWALWVLPPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRA
tr|Q8BMF7                  MKSLWLCWALWVLPPLAGPGAAMTEEQVLSSLLQQLQLSQAPTLDSDADVEEMAIPTHVRS
sp|P57785|LFTB_MOUSE      MKSLWLCWALWVLPPLAGPGAAMTEEQVLSSLLQQLQLSQAPTLDSDADVEEMAIPTHVRS
sp|Q64280|TGF4_MOUSE      MPFLWLCWALWALSIVSLREALTGEQILGSLLQQLQLDQPPVLDKADVEGMVIPSHVRT
*   *****.*.*..   *: * *: *.***:****.: *.** *: * :.***:***:

sp|O00292|TGF4_HUMAN      YVLLRRSHGDRSRGKRFSQSFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLR
sp|O75610|LFTB_HUMAN      YVALLQRSHGDRSRGKRFSQSFREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLR
tr|Q8BMF7                  YVALLQGSHADRSRGKRFSQNFREVAGRFLMSETSTHLLVFGMEQRLPPNSELVQAVLR
sp|P57785|LFTB_MOUSE      YVALLQGSHADRSRGKRFSQNLREVAGRFLMSETSTHLLVFGMEQRLPPNSELVQAVLR
sp|Q64280|TGF4_MOUSE      YVALLQGHSHASRSRGKRFSQNLREVAGRFLVSETSTHLLVFGMEQRLPPNSELVQAVLR
**.*.: *.**.******.:***** *.:*****

sp|O00292|TGF4_HUMAN      FQEPVPKAALHRHGRSLSPRSARARVTVEWLRVRDDGSNRTSLIDSRIVSVHESGWKAFD
sp|O75610|LFTB_HUMAN      FQEPVPKAALHRHGRSLSPRSARARVTVEWLRVRDDGSNRTSLIDSRIVSVHESGWKAFD
tr|Q8BMF7                  FQEPVPRTALRRFERLSPHSARARVTIEWLRVRDGSNRTALIDSRIVSIHESGWKAFD
sp|P57785|LFTB_MOUSE      FQEPVPRTALRRFERLSPHSARARVTIEWLRVRDGSNRTALIDSRIVSIHESGWKAFD
sp|Q64280|TGF4_MOUSE      FQEPVPRTALRRQKRSLSPHSARARVTIEWLRFRDDGSNRTALIDSRIVSIHESGWKAFD
*****.:*:* * * *.:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*

sp|O00292|TGF4_HUMAN      TEAVNFWQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAP--AGLGEPQLEL
sp|O75610|LFTB_HUMAN      TEAVNFWQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAP--AGLGEPQLEL
tr|Q8BMF7                  TEAVNFWQQLSRPRQPLLLQVSVQREHLGPGTWSAHKLVRFAAQGTDPDGKGQGEPOLEL
sp|P57785|LFTB_MOUSE      TEAVNFWQQLSRPRQPLLLQVSVQREHLGPGTWSAHKLVRFAAQGTDPDGKGQGEPOLEL
sp|Q64280|TGF4_MOUSE      TEAVNFWQQLSRPRQPLLLQVSVQREHLGPGTWSSHKLVRFAAQGTDPDGKGQGEPOLEL
*****.:*:* * * *.:*:*:*:*:*:*:*:*:*:*:*:*:*:*

sp|O00292|TGF4_HUMAN      TLDLRDYGAGQDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTC
sp|O75610|LFTB_HUMAN      TLDLDGYGAGQDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTC
tr|Q8BMF7                  TLDLKDYGAGQNCDEVPVTEGTRCCRQEMYLDLQGMKWAENWVLEPPGFLTYECVGSC
sp|P57785|LFTB_MOUSE      TLDLKDYGAGQNCDEVPVTEGTRCCRQEMYLDLQGMKWAENWVLEPPGFLTYECVGSC
sp|Q64280|TGF4_MOUSE      TLDLKDYGAGQNCDEAPVTEGTRCCRQEMYLDLQGMKWAENWVLEPPGFLTYECVGSC
**** * * * *.:*:* * * *.:*:*:*:*:*:*:*:*:*:*:*:*:*:*

sp|O00292|TGF4_HUMAN      QPPEALAFNWPFLGPRQCIASETASLPMIVSIKEGGTRTPQVVSIPNMRVQKSCASDG
sp|O75610|LFTB_HUMAN      QPPEALAFKWPFLLGPRQCIASETDSLPMIVSIKEGGTRTPQVVSIPNMRVQKSCASDG
tr|Q8BMF7                  QLPESLTIGWPFLLGPRQCVASEMTSLPMIVSVKEGGTRTPQVVSIPNMRVQTCSCASDG
sp|P57785|LFTB_MOUSE      QLPESLTIGWPFLLGPRQCVASEMTSLPMIVSVKEGGTRTPQVVSIPNMRVQTCSCASDG
sp|Q64280|TGF4_MOUSE      QLPESLTSRWPFLLGPRQCVASEMTSLPMIVSVKEGGTRTPQVVSIPNMRVQTCSCASDG
* * *.: * * * *.:*:* * * *.:*:*:*:*:*:*:*:*:*:*:*:*:*

sp|O00292|TGF4_HUMAN      LVPRRLQP
sp|O75610|LFTB_HUMAN      LVPRRLQP
tr|Q8BMF7                  LIPRGIDL
sp|P57785|LFTB_MOUSE      LIPRGIDL
sp|Q64280|TGF4_MOUSE      LIPRRLQP
*:* * :

```


FileUp

MSF: 368 Type: P Check: 4364 ..

Name: sp|O00292|TGF4_HUMAN oo Len: 368 Check: 6379 Weight: 0.100
 Name: sp|O75610|LFTB_HUMAN oo Len: 368 Check: 6179 Weight: 0.100
 Name: tr|Q8BMF7 oo Len: 368 Check: 9710 Weight: 0.100
 Name: sp|P57785|LFTB_MOUSE oo Len: 368 Check: 9860 Weight: 0.100
 Name: sp|Q64280|TGF4_MOUSE oo Len: 368 Check: 2236 Weight: 0.100

//

sp O00292 TGF4_HUMAN	MWPLWLCWAL	WVLPLAGPGA	ALTEEQLLGS	LLRQLQLSEV	PVLDRADMEK
sp O75610 LFTB_HUMAN	MQPLWLCWAL	WVLPLASPGA	ALTGEQLLGS	LLRQLQLKEV	PTLDRADMEE
tr Q8BMF7	MKSLWLCWAL	WVLPLAGPGA	AMTEEQVLSS	LLQQLQLSQA	PTLDSADVEE
sp P57785 LFTB_MOUSE	MKSLWLCWAL	WVLPLAGPGA	AMTEEQVLSS	LLQQLQLSQA	PTLDSADVEE
sp Q64280 TGF4_MOUSE	MPFLWLCWAL	WALSIVSLRE	ALTGEQILGS	LLQQLQLDQP	PVLDKADVEG

sp O00292 TGF4_HUMAN	LVIPAHVRAQ	YVLLRRSHG	DRSRGKRFSQ	SFREVAGRFL	ASEASTHLLV
sp O75610 LFTB_HUMAN	LVIPTHVRAQ	YVALLQRSHG	DRSRGKRFSQ	SFREVAGRFL	ALEASTHLLV
tr Q8BMF7	MAIPTHVRSQ	YVALLQGSHA	DRSRGKRFSQ	NFREVAGRFL	MSETSTHLLV
sp P57785 LFTB_MOUSE	MAIPTHVRSQ	YVALLQGSHA	DRSRGKRFSQ	NLREVAGRFL	MSETSTHLLV
sp Q64280 TGF4_MOUSE	MVIPSHVRTQ	YVALLQHSHA	SRSRGKRFSQ	NLREVAGRFL	VSETSTHLLV

sp O00292 TGF4_HUMAN	FGMEQRLPPN	SELVQAVLRL	FQEPVPKAAL	HRHGRLSPRS	AQARVTVEWL
sp O75610 LFTB_HUMAN	FGMEQRLPPN	SELVQAVLRL	FQEPVPKAAL	HRHGRLSPRS	ARARVTVEWL
tr Q8BMF7	FGMEQRLPPN	SELVQAVLRL	FQEPVPRTAL	RRFERLSPHS	ARARVTIEWL
sp P57785 LFTB_MOUSE	FGMEQRLPPN	SELVQAVLRL	FQEPVPRTAL	RRFERLSPHS	ARARVTIEWL
sp Q64280 TGF4_MOUSE	FGMEQRLPPN	SELVQAVLRL	FQEPVPRTAL	RRQKRLSPHS	ARARVTIEWL

sp O00292 TGF4_HUMAN	RVRDDGSNRT	SLIDSRLVSV	HESGWKAFDV	TEAVNFWQQ	SRPRQPLLLQ
sp O75610 LFTB_HUMAN	RVRDDGSNRT	SLIDSRLVSV	HESGWKAFDV	TEAVNFWQQ	SRPRQPLLLQ
tr Q8BMF7	RVREDGSNRT	ALIDSRLVSI	HESGWKAFDV	TEAVNFWQQ	SRPRQPLLLQ
sp P57785 LFTB_MOUSE	RVREDGSNRT	ALIDSRLVSI	HESGWKAFDV	TEAVNFWQQ	SRPRQPLLLQ
sp Q64280 TGF4_MOUSE	RFRDDGSNRT	ALIDSRLVSI	HESGWKAFDV	TEAVNFWQQ	SRPRQPLLLQ

sp O00292 TGF4_HUMAN	VSVQREHLGP	LASGAHKLVR	FASQGAP..A	GLGEPQLELH	TLDLRDYGAQ
sp O75610 LFTB_HUMAN	VSVQREHLGP	LASGAHKLVR	FASQGAP..A	GLGEPQLELH	TLDLGDYGAQ
tr Q8BMF7	VSVQREHLGP	GTWSAHKLVR	FAAQGTPDGK	GQGEPPQLELH	TLDLKDYGAA
sp P57785 LFTB_MOUSE	VSVQREHLGP	GTWSAHKLVR	FAAQGTPDGK	GQGEPPQLELH	TLDLKDYGAA
sp Q64280 TGF4_MOUSE	VSVQREHLGP	GTWSSHKLVR	FAAQGTPDGK	GQGEPPQLELH	TLDLKDYGAA

sp O00292 TGF4_HUMAN	GDCDPEAPMT	EGTRCCRQEM	YIDLQGMKWA	KNWVLEPPGF	LAYECVGTCT
sp O75610 LFTB_HUMAN	GDCDPEAPMT	EGTRCCRQEM	YIDLQGMKWA	ENWVLEPPGF	LAYECVGTCT
tr Q8BMF7	GDCDPEVPVT	EGTRCCRQEM	YIDLQGMKWA	ENWILEPPGF	LTYECVGSCL
sp P57785 LFTB_MOUSE	GDCDPEVPVT	EGTRCCRQEM	YIDLQGMKWA	ENWILEPPGF	LTYECVGSCL
sp Q64280 TGF4_MOUSE	GDCDPEAPVT	EGTRCCRQEM	YIDLQGMKWA	ENWILEPPGF	LTYECVGSCL

sp O00292 TGF4_HUMAN	QPPEALAFNW	PFLGPRQCIA	SETASLPMIV	SIKEGGRTRP	QVVSPLNMRV
sp O75610 LFTB_HUMAN	QPPEALAFKW	PFLGPRQCIA	SETDSLPMIV	SIKEGGRTRP	QVVSPLNMRV

tr Q8BMF7	QLPESLTIGW PFLGPRQCVA SEMTSLPMIV SVKEGGTRP QVVS LPNMRV
sp P57785 LFTB_MOUSE	QLPESLTIGW PFLGPRQCVA SEMTSLPMIV SVKEGGTRP QVVS LPNMRV
sp Q64280 TGF4_MOUSE	QLPESLTSRW PFLGPRQCVA SEMTSLPMIV SVKEGGTRP QVVS LPNMRV
sp O00292 TGF4_HUMAN	QKSCASDGA LVPRRLQP
sp O75610 LFTB_HUMAN	QKSCASDGA LVPRRLQP
tr Q8BMF7	QTCSCASDGA LIPRGIDL
sp P57785 LFTB_MOUSE	QTCSCASDGA LIPRGIDL
sp Q64280 TGF4_MOUSE	QTCSCASDGA LIPRR LQP